

Schreiber, David

136374

From: Swope, Sheridan  
Sent: Friday, October 22, 2004 3:41 PM  
To: STIC-Biotech/ChemLib  
Cc: Schreiber, David  
Subject: 09/980,881

Please forward to David Schreiber

David,

For 09/980,881,

pls search and interference search:

SID 9 against the NT and AA data bases, wherein the maximum length of the polypeptide hit is 19 amino acids and the maximum length of the polynucleotide hit is 57 nucleotides.

pls interference search only:

SID 1, residues 18-1097, against the NT and AA data bases  
SID 2 full-length regular and oligo against the NT and AA data bases  
SID 3 full-length regular and oligo against the NT and AA data bases  
SID 4 full-length regular and oligo against the NT and AA data bases

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E02B71 Remsen Bld (Office)  
E02C70 Remsen Bld (Mailbox)

PD 4/30/99

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10/28/04

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2004, 23:09:56 ; Search time 111 Seconds  
(without alignments)  
45.245 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 662259

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1980s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	14	3 AAB11461	Aab11461 Human bra
2	35	50.0	9	2 AAY55419	Aay55419 HLA bindi
3	35	50.0	17	2 AAW62069	Aaw62069 Human lun
4	32	45.7	15	5 ABB75868	Abb75868 Human pho
5	31	44.3	14	4 AAM971138	Aam971138 Human pep
6	31	44.3	18	5 ABG71595	Abg71595 S. cerevi
7	30	42.9	14	3 AAB26736	Aab26736 ATM kinas
8	30	42.9	14	3 AAB24149	Aab24149 Rat megli
9	30	42.9	14	4 AAG64287	Aag64287 Rat megli
10	30	42.9	15	6 ABR30640	Abr30640 Human can
11	30	42.9	15	6 ABR30899	Abr30899 Human can
12	30	42.9	15	6 ABR31213	Abr31213 Human can
13	30	42.9	15	6 ABR31621	Abr31621 Human can
14	29	41.4	10	7 ADD94616	Add94616 Human SIM
15	29	41.4	14	4 AAW48905	Aaw48905 Cyclic pe
16	29	41.4	15	4 AAB84887	Aab84887 Human gal
17	29	41.4	15	5 ABG99831	Abg99831 Conus sp
18	29	41.4	17	8 ADK12493	Adk12493 Antigenic
19	29	41.4	18	2 AAR49494	Aar49494 PAI-1 pos
20	29	41.4	19	2 AAW65054	Aaw65054 E. tenell
21	28	40.0	5	5 AAG69227	Abg69227 Protein S
22	28	40.0	5	7 ADE44908	Ade44908 Structura
23	28	40.0	8	4 AAM22269	Aam22269 HIV pepti
24	28	40.0	8	4 ABP13991	Abp13991 HIV A02 s
25	28	40.0	8	4 ABP16394	Abp16394 HIV A24 s

26	28	40.0	9	4 AAM23273	Aam23273 HIV pepti
27	28	40.0	9	4 AAM22955	Aam22955 HIV pepti
28	28	40.0	9	4 AAM22911	Aam22911 HIV pepti
29	28	40.0	9	4 AAM23272	Aam23272 HIV pepti
30	28	40.0	9	4 AAM23288	Aam23288 HIV pepti
31	28	40.0	9	4 AAM23288	Aam23288 HIV pepti
32	28	40.0	9	4 AAM23274	Aam23274 HIV pepti
33	28	40.0	9	4 AAM23271	Aam23271 HIV pepti
34	28	40.0	9	4 AAM22257	Aam22257 HIV pepti
35	28	40.0	9	4 ABP14004	Abp14004 HIV A02 s
36	28	40.0	9	6 ABR58752	Abt58752 Alzheimer
37	28	40.0	9	7 ADC71090	Adc71090 HLA motif
38	28	40.0	9	7 ADC70982	Adc70982 HLA motif
39	28	40.0	9	8 ADN32071	Adn32071 Human Alz
40	28	40.0	9	8 ADN63663	Adn63663 HLA bindi
41	28	40.0	10	2 AAY45249	Aay45249 HIV-1 (IA
42	28	40.0	10	4 ABP21883	Abp21883 HIV A03 m
43	28	40.0	10	4 ABP23711	Abp23711 HIV A11 m
44	28	40.0	10	4 ABP16403	Abp16403 HIV A24 s
45	28	40.0	10	4 ABP14009	Abp14009 HIV A02 s

ALIGNMENTS

RESULT 1  
AAB11461  
ID AAB11461 standard; protein; 14 AA.  
XX  
AC AAB11461;  
XX  
01-MAR-2001 (first entry)  
XX  
Human brain carboxypeptidase B protein SEQ ID NO 9.  
XX  
Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase;  
KW treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine;  
KW cerebroprotective; antialzheimers; neuroprotective;  
KW hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage;  
KW Down's syndrome; head trauma.  
XX  
Homo sapiens.  
XX  
WO200066717-A1.  
XX  
09-NOV-2000.  
XX  
01-MAY-2000; 2000WO-JP002878.  
XX  
30-APR-1999; 99JP-00125169.  
XX  
(MATS/) MATSUMOTO A.  
XX  
Matsumoto A;  
XX  
WPI; 2000-687534/67.  
XX  
Human brain carboxypeptidase B isolated from the hippocampus useful for  
screening agents for the treatment of Alzheimer's and other brain  
disorders.  
XX  
Example 4; Page 78; 84pp; Japanese.  
XX  
This invention describes a novel protein with peptidase activity against  
brain beta-amyloid precursor protein which has been isolated from human  
hippocampus and which has cerebroprotective, antialzheimers, neurotropic,  
neuroprotective and hemostatic activity and which can be used as a  
vaccine or for gene therapy. The protein, and compounds identified by  
screening as promoters or inhibitors of its activity, are used to  
regulate beta-amyloid accumulation in the brain and treat or prevent  
diseases in which this occurs, such as Alzheimer's, senile dementia,  
inherited cerebral hemorrhage, Down's syndrome, and head trauma  
XX

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SQ      Sequence 14 AA;
Query Match      100.0%; Score 70; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNPPVEKLLPLSLK 14
        |||||
Db      1 SNPPVEKLLPLSLK 14

RESULT 2
AAV55419
ID      AAV55419 standard; peptide; 9 AA.
XX
AC      AAV55419;
XX
DT      17-JAN-2000 (first entry)
XX
DE      HLA binding plu-1 peptide.
XX
Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
KW      breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
KW      therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      WO9949034-A1.
XX
PD      30-SEP-1999.
XX
PF      19-MAR-1999; 99WO-GB000866.
XX
PR      20-MAR-1998; 98GB-00005877.
XX
PA      (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI      Taylor-Papadimitriou J;
XX
WPI; 1999-591090/50.
XX
New nucleic acid encoding the cancer-associated polypeptide plu-1, for
PT      diagnosis, treatment and prevention of cancer, especially of breast and
PT      ovary.
XX
Example 2; Fig 12; 173pp; English.
XX
The invention relates to a human cancer-associated polypeptide plu-1. The
CC      plu-1 polypeptide can be recombinantly expressed by standard recombinant
CC      methodology. Detection of the plu-1 nucleic acid or the polypeptide is
CC      used for the following: (i) diagnosis (including imaging) and prognosis
CC      of, and determination of susceptibility to, cancer, specifically ovarian
CC      or breast cancer; and ii) treating cancer (by inducing an immune response
CC      against cancer cells, e.g. as a vaccine, or by antisense inhibition).
CC      Antigens derived from the polypeptide are used to generate activated
CC      cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the
CC      patient for treatment of cancer. The polypeptide may also be used to
CC      identify inhibitors of plu-1 activity. Fragments of the polypeptide, and
CC      antibodies raised against plu-1, are useful as assay and imaging agents,
CC      also therapeutically (to induce an anti-idiotypic response or where
CC      conjugated to cytotoxic agents). The plu-1 antigen is expressed more
CC      commonly in breast tumors than some known tumor antigens. Sequences
CC      AAV55320-629 represent predicted peptides from the plu-1 polypeptide which
CC      may bind to the human class I alleles B27, A2, A3 and A11
XX
SQ      Sequence 9 AA;
Query Match      50.0%; Score 35; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PVEKLLPL 11
        |||||
Db      1 PVEKLLPL 11

us-09-980-881a-9.rag
Db      1 PLEXILPL 8
        |:|:|

RESULT 3
AAW62069
ID      AAW62069 standard; peptide; 17 AA.
XX
AC      AAW62069;
XX
DT      14-SEP-1998 (first entry)
XX
DE      Human lung tissue gene LU103 protein fragment 1.
XX
Human; lung tissue gene; LU103; detection; lung cancer; diagnosis.
XX
OS      Homo sapiens.
XX
PN      WO9820143-A1.
XX
PD      14-MAY-1998.
XX
PF      05-NOV-1997; 97WO-US020680.
XX
PR      05-NOV-1996; 96US-00744211.
XX
PA      (ABBO ) ABBOTT LAB.
XX
Cohen M, Friedman PN, Gordon J, Hodges SC, Klass MR;
PI      Kratochvill JD, Roberts-Rapp L, Russell JC, Stroupe SD;
XX
WPI; 1998-286957/25.
XX
Lung tissue derived polynucleotide LU103 - useful to detect, diagnose,
PT      stage, monitor, prognosis, prevent, treat or determine pre-disposition to
PT      lung disease, e.g. lung cancer.
XX
Disclosure; Page 70; 86pp; English.
XX
The present sequence represents a protein fragment from lung tissue gene
CC      LU103. A method has been developed for detecting the presence of a target
CC      LU103 polynucleotide in a test sample, comprising: (a) contacting the
CC      sample with at least 1 LU103-specific polynucleotide, and (b) detecting
CC      the target LU103 polynucleotide in the test sample, where the LU103
CC      polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519
CC      bp nucleic acid sequence given in AAV38066 to AAV38070. The methods and
CC      products of the present invention may be used to detect, diagnose, stage,
CC      monitor, prognosis, prevent, treat or determine the predisposition
CC      diseases and conditions of the lung, e.g. lung cancer
XX
SQ      Sequence 17 AA;
Query Match      50.0%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      4 PVEKLLPLSL 13
        ||:|:|
Db      6 PVDKLAFLPL 15

RESULT 4
ABB75868
ID      ABB75868 standard; peptide; 15 AA.
XX
AC      ABB75868;
XX
DT      01-JUL-2002 (first entry)
XX
DE      Human phospholipase 9 peptide fragment.
XX
Phospholipase; human; enzyme; tumour; haemopathy; HIV infection;
KW      immunological disease; inflammation; antitumour; haemostatic; anti-HIV;

```

virucide; immunomodulatory; antiinflammatory; gene therapy.

Homo sapiens.

WO200183537-A1.

08-NOV-2001.

28-APR-2001; 2001WO-CN000629.

29-APR-2000; 2000CN-00115568.

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Mao Y, Xie Y;

WPI; 2002-055456/07.

Human phospholipase 9 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammations.

Example 5; Page 19; 39pp; Chinese.

The present invention relates to human phospholipase 9 (see ABB75867).

The enzyme and its coding sequence are useful in the diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various inflammations (all claimed). The present sequence is an N-terminal peptide fragment of the phospholipase, which was used in a method from the invention

Sequence 15 AA;

Query Match 45.7%; Score 32; DB 5; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVEKLLP 10  
DB 7 PVEKLLP 13

RESULT 5

AA97138

ID AAM97138 standard; peptide; 14 AA.

AC AAM97138;

XX 24-JAN-2002 (first entry)

DE Human peptide #413 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.  
XX Disclosure; Page 3758; 4143pp; English.  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases.  
XX The present sequence is a peptide encoded by one such oligonucleotide.  
XX The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms

Sequence 14 AA;

Query Match 44.3%; Score 31; DB 4; Length 14;  
Best Local Similarity 46.2%; Pred. No. 2.8e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPPVEKLLPLSL 13  
DB 2 SNPKGSQMQLSL 14

RESULT 6

ABG71595

ID ABG71595 standard; peptide; 18 AA.

XX ABG71595;

XX 08-JAN-2003 (first entry)

DE S. cerevisiae peptide useful for replacing G. multiflorum rGel Y4.

XX Modified protein; reduced antigenicity; modified toxin; gelonin; designer toxin; immunotoxin; proteinaceous compound; cancer; microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease; hyperproliferative disorder; leukaemia; arthritis; inflammatory disease; cardiovascular disease; diabetes; pathogenic disease; cytostatic; antiarthritic; antiinflammatory; cardiant; antidiabetic; virucide; protozoacide; fungicide; recombinant gelonin; rGel; antigenic; Y4.

XX Saccharomyces cerevisiae.

XX WO200269886-A2.

XX 12-SEP-2002.

XX 12-FEB-2002; 2002WO-US004195.

XX 12-FEB-2001; 2001US-0268402P.

XX (RERE-) RES DEV FOUND.

XX Rosenblum MG, Cheung L;

XX WPI; 2002-750431/81.

XX Generating a modified protein with reduced antigenicity for treating  
 PT cancer, AIDS, autoimmune diseases, comprises identifying a protein region  
 PT antigenic in the first subject using antiserum from either the first or a  
 PT second subject.

XX Example 3; Page 114; 176pp; English.

CC The present invention relates to a method of generating a modified  
 CC protein with reduced antigenicity while maintaining its biological  
 CC activity. The method comprises identifying a region of the protein that  
 CC is antigenic in a first subject using antiserum from either the first  
 CC subject or a second subject of the same species as the first subject. In  
 CC particular the invention discloses modified toxin compounds, for example  
 CC gelonin toxin derived from Gelonium multiflorum, that are truncated  
 CC and/or possess reduced antigenicity. Such designer toxins have  
 CC immunotoxins. The method, and preventative benefits, particularly as  
 CC proteinaceous compounds with less antigenicity. The immunotoxin and  
 CC gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain,  
 CC skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,  
 CC bone, bone marrow, head and neck, cervical, oesophagus, eye, gall  
 CC bladder, kidney, adrenal glands, heart, colon, or blood cancer. The  
 CC compositions of the invention are also useful for treating microbial  
 CC pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune  
 CC diseases, hyperproliferative disorders including cancer, leukaemias,  
 CC arthritis, inflammatory diseases, cardiovascular diseases, pathogenic  
 CC diseases, and diabetes. The method provides less antigenic proteins,  
 CC peptides and polypeptides, which are more effective than prior art. The  
 CC present sequence represents a potential replacement peptide for G.  
 CC multiflorum recombinant gelonin (rGel) antigenic sequence Y4

XX Sequence 18 AA;

Query Match 44.3%; Score 31; DB 5; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 3.7e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLPLSLK 14  
 ||| : |||  
 Db 6 PLVESVIVLSLK 17

RESULT 7  
 AAB26736  
 ID AAB26736 standard; peptide; 14 AA.

XX AAB26736;

XX 12-JAN-2001 (first entry)

XX ATM kinase substrate recognition peptide SEQ ID 31.

XX Ataxia telangiectasia-mutated; ATM; kinase; ataxia telangiectasia;  
 KW tumour; cardiovascular disease; restenosis; revascularisation; obesity;  
 KW retroviral infection; HIV; human T cell leukaemia virus; HTLV.

XX Unidentified.

XX WO200047760-A2.

XX 17-AUG-2000.

XX 09-FEB-2000; 2000WO-US003386.

XX 10-FEB-1999; 99US-00248061.

XX 21-SEP-1999; 99US-00400653.

XX (SUJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Kastan M, Canman C, Kim S, Lim D;

DR WPI; 2000-559218/51.

XX Identifying proteins with ataxia telangiectasia-mutated kinase substrate  
 PT recognition sequences, useful for investigating ATM kinase specificity  
 PT and treating human T cell leukemia virus.

XX Example 3; Page 77; 106pp; English.

CC This invention relates to a method for identifying an ataxia  
 CC telangiectasia-mutated (ATM) kinase substrate recognition sequence in a  
 CC protein. The method comprises contacting an ATM kinase with a fusion  
 CC peptide containing a structural portion and a candidate ATM kinase  
 CC substrate recognition sequence, where the fusion protein does not contain  
 CC a sequence of 14 amino acids represented in AAB26709 which is a p53  
 CC derived ATM kinase substrate peptide. Ataxia telangiectasia (AT) is a  
 CC rare autosomal recessive multi-system disorder, one of the clinical  
 CC manifestations is an increased risk of cancer. The gene mutated in AT,  
 CC ATM is related to the phosphatidylinositol 3-kinase (PI-3-K) family of  
 CC proteins. The method of the invention can be used to investigate ATM  
 CC kinase specificity and to identify ATM target proteins other than p53.  
 CC The modulation of ATM activity may be used to treat cancer (e.g. to  
 CC radiosensitise tumours), cardiovascular disease (e.g. restenosis),  
 CC revascularisation, obesity and retroviral infections (e.g. HIV and  
 CC especially human T cell leukaemia virus (HTLV). The present sequence  
 CC represents an ATM kinase substrate recognition peptide sequence  
 CC identified in the invention

XX Sequence 14 AA;

Query Match 42.9%; Score 30; DB 3; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 4.1e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLPLSL 12  
 ||| : |||  
 Db 4 PPVSQELPCS 13

RESULT 8  
 AAB24149  
 ID AAB24149 standard; peptide; 14 AA.

XX AAB24149;

XX 30-JAN-2001 (first entry)

XX Rat megin domain peptide SEQ ID NO:17.

XX Megsin; mesangium-predominant gene; serpin regulated; nephropathy; IGA;  
 KW immunoglobulin A; detection; renal function; renal disorder; diagnosis;  
 KW biological sample; blood; urine.

XX Rattus norvegicus.

XX WO200057189-A1.

XX 28-SEP-2000.

XX 17-MAR-2000; 2000WO-JP001646.

XX 19-MAR-1999; 99JP-00075305.

XX 28-OCT-1999; 99JP-00306623.

XX (KURO/) KUROKAWA K.

XX (FUSO ) FUSO PHARM IND LTD.

XX (MIYA/) MIYATA T.

XX Miyata T;

XX WPI; 2000-611642/58.

XX Evaluating renal function comprises assaying megin protein in biological  
 PT sample.

XX PS Example 2; Page 29; 93pp; Japanese.

XX CC The present invention describes a method for evaluating renal function.

XX CC The method comprises assaying megin protein in biological sample. Also

XX CC described are: (1) use of an anti-megsin protein antibody for diagnosing

XX CC renal function; and (2) a kit for detecting megin protein comprising:

XX CC (a) anti-megsin protein antibody attached to solid magnetic particles; (b)

XX CC direct or indirect fixing for the antibody to the particles; and (c) a

XX CC magnet. The process is useful for evaluating renal function and

XX CC diagnosing renal disorders by assaying megin protein in biological

XX CC samples (preferably urine or blood). The process is reproducible and

XX CC gives accurate results. The present sequence represents a rat megin

XX CC domain peptide, which is used in an example from the present invention

XX SQ Sequence 14 AA;

Query Match 42.9%; Score 30; DB 3; Length 14;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VEKLLPLS 12

DB 5 VEKLLPES 12

RESULT 9

AAG64287

ID AAG64287 standard; peptide; 14 AA.

XX AC AAG64287;

XX DT 21-SEP-2001 (first entry)

XX DE Rat megin peptide fragment.

XX KW Rat; megin; renal mesangial cell; mesangium proliferative nephritis.

XX OS Rattus norvegicus.

XX PN WO200148019-A1.

XX PD 05-JUL-2001.

XX PF 26-DEC-2000; 2000WO-JP009251.

XX PR 28-DEC-1999; 99JP-00373677.

XX PA (KURO/) KUROKAWA K.

XX PA (MIYA/) MIYATA T.

XX PI Miyata T;

XX DR WPI; 2001-425651/45.

XX PT New antibody recognizing a partial sequence of rat megin protein for

XX PT diagnosis of mesangium proliferative nephritis.

XX PS Claim 1; Page 29; 63pp; Japanese.

XX CC The present invention relates to a novel antibody which recognises a

XX CC peptide (the present sequence) consisting of residues 341-354 of rat

XX CC megin protein. Megsin is highly expressed in renal mesangial cells and

XX CC its level is elevated in mesangium proliferative nephritis. Assay of the

XX CC serum or urine level using the antibody is therefore indicative of this

XX CC type of disorder. For the full-length rat megin protein see AAG64286

XX SQ Sequence 14 AA;

Query Match 42.9%; Score 30; DB 4; Length 14;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VEKLLPLS 12

DB 5 VEKLLPES 12

RESULT 9

AAG64287

ID AAG64287 standard; peptide; 14 AA.

XX AC AAG64287;

XX DT 21-SEP-2001 (first entry)

XX DE Rat megin peptide fragment.

XX KW Rat; megin; renal mesangial cell; mesangium proliferative nephritis.

XX OS Rattus norvegicus.

XX PN WO200148019-A1.

XX PD 05-JUL-2001.

XX PF 26-DEC-2000; 2000WO-JP009251.

XX PR 28-DEC-1999; 99JP-00373677.

XX PA (KURO/) KUROKAWA K.

XX PA (MIYA/) MIYATA T.

XX PI Miyata T;

XX DR WPI; 2001-425651/45.

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XX PT diagnosis of mesangium proliferative nephritis.

XX PS Claim 1; Page 29; 63pp; Japanese.

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XX CC its level is elevated in mesangium proliferative nephritis. Assay of the

XX CC serum or urine level using the antibody is therefore indicative of this

XX CC type of disorder. For the full-length rat megin protein see AAG64286

XX SQ Sequence 14 AA;

Query Match 42.9%; Score 30; DB 4; Length 14;

Best Local Similarity 87.5%; Pred. No. 4.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VEKLLPLS 12

DB 5 VEKLLPES 12

RESULT 10

ABR30640

ID ABR30640 standard; peptide; 15 AA.

XX AC ABR30640;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 83P4B8 HLA peptide #1702.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX XX (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response in

XX PT cancer patients.

XX PS Claim 13; Page 478; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and

XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

XX CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or

XX CC detection of genes, mRNAs or their fragments, as reagents for the

XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of

XX CC directing the expression of the protein, as tools for modulating or

XX CC inhibiting the expression of genes and/or translation of transcripts, and

XX CC as therapeutic agents. The proteins and peptides are useful as

XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present

XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX CC from the invention

XX SQ Sequence 15 AA;

Query Match 42.9%; Score 30; DB 6; Length 15;

Best Local Similarity 50.0%; Pred. No. 4.5e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPEVKLLPLSL 13

DB 1 NQPEKAIIMQL 12

RESULT 11

ABR30899

ID ABR30899 standard; peptide; 15 AA.

XX AC ABR30899;

XX 19-MAY-2003 (first entry)  
 XX Human cancer-related protein 83P4B8 HLA peptide #1961.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 KW Homo sapiens.  
 XX WO200283921-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US011654.  
 XX 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX Claim 13; Page 483; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX Sequence 15 AA;  
 SQ Query Match 42.9%; Score 30; DB 6; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 NPPVEKLLPLSL 13  
 Db | | | | : : |  
 1 NQPVEXAIIQMQL 12  
 RESULT 12  
 ABR31213  
 ID ABR31213 standard; peptide; 15 AA.  
 XX ABR31213;  
 AC ABR31213;  
 XX 19-MAY-2003 (first entry)  
 XX Human cancer-related protein 83P4B8 HLA peptide #2275.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 XX

PN WO200283921-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US011654.  
 XX 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX Claim 13; Page 488; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX Sequence 15 AA;  
 SQ Query Match 42.9%; Score 30; DB 6; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 NPPVEKLLPLSL 13  
 Db | | | | : : |  
 1 NQPVEXAIIQMQL 12  
 RESULT 13  
 ABR31621  
 ID ABR31621 standard; peptide; 15 AA.  
 XX ABR31621;  
 AC ABR31621;  
 XX 19-MAY-2003 (first entry)  
 XX Human cancer-related protein 83P4B8 HLA peptide #2683.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 XX WO200283921-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US011654.  
 XX 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX

PA (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
XX Claim 13; Page 495; 1021pp; English.  
PS  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;  
Query Match 42.9%; Score 30; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 4.5e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 NPPVEKLLPLSL 13  
DB 4 NQPVKAIIMQL 15  
RESULT 14  
ADD94616  
ID ADD94616 standard; peptide; 10 AA.  
XX  
AC ADD94616;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human SIMP-derived peptide 136.  
XX  
KW source of immunodominant MHC-associated peptide; SIMP; MHC;  
KW major histocompatibility complex; human leukocyte antigen; HLA;  
KW cytostatic; immunosuppressive; antisense therapy; gene therapy; cancer;  
KW lung cancer; intestine cancer; sarcoma; prostate cancer;  
KW testicular cancer; breast cancer; melanomas; pancreatic cancer;  
KW haematological cancer; immune response; lymphoid cell proliferation;  
KW autoimmune disease; transplant rejection; SIMP-derived peptide; human.  
XX  
OS Homo sapiens.  
XX  
PN W02003054008-A2.  
XX  
XX 03-JUL-2003.  
XX  
XX 18-DEC-2002; 2002WO-CA001967.  
XX  
XX 20-DEC-2001; 2001US-00028384.  
XX  
XX (COMP-) COMPATIGENE INC.  
XX  
XX Perreault C, McBride K;  
XX  
XX WPI; 2003-559122/52.  
XX  
XX New human source of immunodominant MHC-associated peptide (SIMP) nucleic  
PT acids and proteins, useful for diagnosing and treating cancers, e.g. lung  
or breast cancer, or for suppressing an immune response in an autoimmune  
disease.  
Claim 24; Page 19; 66pp; English.  
This invention relates to a novel isolated or purified human protein, termed source of immunodominant major histocompatibility complex (MHC)-associated peptide (SIMP), which is expressed ubiquitously in human cells, where the protein has the potential of generating several protein fragments binding with high affinity to a human leukocyte antigen (HLA) molecule. The invention may allow development of therapeutics with cytostatic or immunosuppressive activity or provide sequences useful for antisense therapy or gene therapy. The source of immunodominant MHC-associated peptide (SIMP) nucleic acids, proteins and fragments are useful for diagnosing and treating cancers, for example lung cancer, intestine cancer, sarcomas, prostate cancer, testicular cancer, breast cancer, melanomas, pancreatic cancer or haematological cancer. The SIMP proteins are also useful for modulating an immune response. Decreasing lymphoid cell proliferation is useful for suppressing an immune response responsible for an autoimmune disease or a transplant rejection. The present sequence is that of a human SIMP-derived peptide (with a high affinity binding motif for HLA molecules) of the invention.  
Sequence 10 AA;  
Query Match 41.4%; Score 29; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NPPVE 6  
DB 4 NPPVE 8  
RESULT 15  
AAW48905  
ID AAW48905 standard; peptide; 14 AA.  
XX  
AC AAW48905;  
XX  
DT 23-SEP-1998 (first entry)  
XX  
DE Cyclic peptide gramicidin S14 analogue Y2/F2 V3/L3.  
XX  
KW Cyclic; gramicidin S; GS; beta-pleated structure; therapeutic index; hemolysis; Gram-positive bacteria; Gram-negative bacteria; fungi; mycoplasma; food additive; antimicrobial activity.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1..14 /note= "Residue 1 is in a peptide linkage with residue 14"  
FT Misc-difference 4 /note= "D-form residue"  
FT Misc-difference 6 /note= "D-form residue"  
FT Misc-difference 13 /note= "D-form residue"  
FT  
XX W09816549-A1.  
XX  
XX 23-APR-1998.  
XX  
XX 10-OCT-1997; 97WO-US018693.  
XX  
XX 11-OCT-1996; 96US-0028315P.  
XX  
XX (PENC-) PENCE INC.  
XX  
XX (DEHL/) DEHLINGER P J.  
XX

PI Kondejewski LH, Hodges RS, Wishart DS, Hancock REW, McElhaney R;  
 PI Prenner EJ, Lewis RNAH;  
 XX  
 XX WPI; 1998-251231/22.  
 XX  
 XX Cyclic peptide analogues of gramicidin S with broad spectrum  
 PT antimicrobial activity - and reduced haemolytic activity, have beta-  
 PT plated sheet structure disrupted or eliminated by amino acid  
 PT substitutions.  
 XX  
 XX  
 PS Disclosure; Page 45; 88pp; English.  
 XX  
 XX The invention provides for cyclic peptide analogues of gramicidin S14  
 CC (GS14; AAM48876), such as the present one. These cyclic peptide GS14  
 CC analogues do not have the beta-pleated structure present in Gramicidin S  
 CC (GS). These analogues are claimed to have an advantage over GS as they  
 CC have broad spectrum antimicrobial activity and an increased therapeutic  
 CC index because they lack the hemolytic effect of GS. The cyclic peptide  
 CC GS14 analogues are also claimed to be useful therapeutically in human or  
 CC veterinary medicine to kill or inhibit Gram-positive and -negative  
 CC bacteria, fungi and mycoplasma. They may also be used to control  
 CC mycoplasma contamination of cultured cells and as food additives  
 XX  
 XX  
 SQ Sequence 14 AA;  
  
 Query Match 41.4%; Score 29; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 6.1e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 7 KLLPLSLK 14  
 |||||  
 Db 4 KLFPLK 11  
  
 Search completed: October 27, 2004, 01:02:51  
 Job time : 116 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 00:54:50 ; Search time 42 Seconds  
(without alignments)  
22.106 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 179518

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/6CTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

pred, No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	50.0	17	2	US-08-964-725-15
2	33	47.1	12	4	US-09-007-288E-88
3	30	42.9	14	3	US-09-400-653A-31
4	30	42.9	14	3	US-09-248-061B-27
5	29	41.4	18	2	US-08-480-190-204
6	29	41.4	18	2	US-08-488-379-204
7	29	41.4	18	4	US-08-475-399A-204
8	29	41.4	18	4	US-08-077-255A-204
9	29	41.4	18	5	PCT-US93-07545-204
10	28	40.0	5	1	US-08-477-509B-13
11	28	40.0	5	3	US-08-482-085B-13
12	28	40.0	5	3	US-09-444-791A-13
13	28	40.0	15	1	US-08-230-047-31
14	28	40.0	15	3	US-09-141-882A-10
15	28	40.0	15	3	US-09-452-142-10
16	28	40.0	17	4	US-09-355-398C-2
17	28	40.0	18	4	US-09-355-398C-5
18	28	40.0	19	3	US-08-943-173-8
19	27	38.6	10	3	US-08-836-561-51
20	27	38.6	10	4	US-09-434-122-51
21	27	38.6	16	1	US-08-185-432-14
22	27	38.6	16	4	US-09-715-923-8
23	26.5	37.9	16	3	US-08-602-999A-204
24	26.5	37.9	16	4	US-09-500-124-204
25	26	37.1	9	1	US-08-615-181-100
26	26	37.1	10	4	US-08-983-157B-8
27	26	37.1	10	4	US-09-653-465B-11

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 519, Appl  
Sequence 43, Appl  
Sequence 121, Appl  
Sequence 79, Appl  
Sequence 1, Appl  
Sequence 15, Appl  
Sequence 100, Appl  
Sequence 322, Appl  
Sequence 156, Appl  
Sequence 322, Appl  
Sequence 156, Appl  
Sequence 33, Appl  
Sequence 71, Appl  
Sequence 34, Appl

ALIGNMENTS

RESULT 1  
US-08-964-725-15  
; Sequence 15, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.PI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: No. 5939265e
US-08-964-725-15

Query Match      50.0%; Score 35; DB 2; Length 17;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PVEKLLPLSL 13
Db 6 PVDKLAFLPL 15

RESULT 2
US-09-007-288E-88
; Sequence 88, Application US/09007288E
; Patent No. 6495357
; GENERAL INFORMATION:
; APPLICANT: Fuglsang, Claus
; APPLICANT: Oktels, Jens
; APPLICANT: Petersen, Dorte
; APPLICANT: Patkar, Shamkant
; APPLICANT: Thellersen, Marianne
; APPLICANT: Svenden, Allan
; APPLICANT: Borch, Kim
; APPLICANT: Royer, John
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Halkier, Torben
; APPLICANT: Vind, Jesper
; APPLICANT: Jorgensen, Steen
; TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes
; FILE REFERENCE: 4455-404-US
; CURRENT APPLICATION NUMBER: US/09/007,288E
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide addition
US-09-007-288E-88

Query Match      47.1%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 3 PPRRLPLFIS 12

RESULT 3
US-09-400-653A-31
; Sequence 31, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/1F142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-400-653A-31

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 4
US-09-248-061B-27
; Sequence 27, Application US/09248061B
; Patent No. 6387640
; GENERAL INFORMATION:
; APPLICANT: Kastan, M.
; APPLICANT: Canman, C.
; APPLICANT: Kim, S-T.
; APPLICANT: Lim, D-S.
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 2427/0F142
; CURRENT APPLICATION NUMBER: US/09/248,061B
; CURRENT FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-27

Query Match      42.9%; Score 30; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12
Db 4 PPVSQELPCS 13

RESULT 5
US-08-480-190-204
; Sequence 204, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-480-190-204

Query Match 41.4%; Score 29; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | |  
Db 3 PYKEVPLS 11

RESULT 7  
US-08-475-399A-204  
; Sequence 204, Application US/08475399A  
; Patent No. 6509033  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chiciz, Roman M.  
; APPLICANT: Vignali, Dario A.A.  
; APPLICANT: Hedley, Mary L.  
; APPLICANT: Stern, Lawrence J.  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 276  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: Fast-SEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,399A  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: 15-JUN-1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: 11-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00246/168003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-507  
; TELEFAX: 617/542-890  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-475-399A-204

Query Match 41.4%; Score 29; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | |  
Db 3 PYKEVPLS 11

RESULT 8

; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-480-190-204

Query Match 41.4%; Score 29; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLLPLS 12  
| | | | |  
Db 3 PYKEVPLS 11

RESULT 6  
US-08-488-379-204  
; Sequence 204, Application US/08488379  
; Patent No. 5880103  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chiciz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,379  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:

US-08-077-255A-204  
; Sequence 204, Application US/08077255A  
; Patent No. 6696061  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/077,255A  
; FILING DATE: June 15, 1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-077-255A-204  
Query Match 41.4%; Score 29; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 PVEKLLPLS 12  
| | | : | | |  
Db 3 PYKEVPLS 11  
| | | : | | |  
RESULT 9  
PCT-US93-07545-204  
; Sequence 204, Application PC/TUS9307545  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 273  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07545  
; FILING DATE: 19930811  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 204:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
PCT-US93-07545-204  
Query Match 41.4%; Score 29; DB 5; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 PVEKLLPLS 12  
| | | : | | |  
Db 3 PYKEVPLS 11  
| | | : | | |  
RESULT 10  
US-08-477-509B-13  
; Sequence 13, Application US/08477509B  
; Patent No. 5770697  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W  
; APPLICANT: Dorman, Mary A  
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,509B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-13

Query Match 40.0%; Score 28; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 11  
US-08-482-085B-13  
Sequence 13, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
UNITS OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7  
Db 1 PPVEK 5

RESULT 12  
US-09-444-791A-13  
Sequence 13, Application US/09444791A  
Patent No. 6355776  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
UNITS OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,791A  
FILING DATE: 22-NOV-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-444-791A-13

Query Match 40.0%; Score 28; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
Db 1 PPVEK 5

## RESULT 13

US-08-230-047-31  
Sequence 31, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:  
APPLICANT: Searfoss III, George H.  
APPLICANT: Ivashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcoia Road, 3c43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-31

Query Match 40.0%; Score 28; DB 1; Length 15;  
Best Local Similarity 44.4%; Pred. NO. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPL 11  
Db 6 PPLPQFLPW 14

## RESULT 14

US-09-141-882A-10  
Sequence 10, Application US/09141882A  
Patent No. 6022540  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/141.882A  
FILING DATE: herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/057,928  
FILING DATE: September 4, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: SEMIONOW, R.  
REGISTRATION NUMBER: 39,022  
REFERENCE/DOCKET NUMBER: 640100-249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: peptide  
US-09-141-882A-10  
Query Match 40.0%; Score 28; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 NPPVEKLL 9  
Db 6 NPPPEEFL 13  
RESULT 15  
US-09-452-142-10  
Sequence 10, Application US/09452142  
Patent No. 6379553  
GENERAL INFORMATION:  
APPLICANT: Bruder, S. and Jaiswal, N.  
TITLE OF INVENTION: Ligands That Modulate  
TITLE OF INVENTION: Differentiation of Mesenchymal Stem Cells  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/452,142  
FILING DATE: 01-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/141,882  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: SEMIONOW, R.  
REGISTRATION NUMBER: 39,022  
REFERENCE/DOCKET NUMBER: 640100-249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: <Unknown>  
TOPOLOGY: LINEAR  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-452-142-10

Query Match 40.0%; Score 28; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPPVEXLL 9  
||| |:  
Db 6 NPPPEEFL 13

Search completed: October 27, 2004, 01:06:58  
Job time : 45 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:05:26 ; Search time 1033 Seconds  
(without alignments)  
4.388 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 260209

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	50.0	9	US-10-334-726-111	Sequence 111, App
2	33	47.1	12	US-10-232-544-88	Sequence 88, Appl
3	30	42.9	14	US-10-024-123-31	Sequence 31, Appl
4	29	41.4	15	US-10-072-602B-616	Sequence 616, App
5	29	41.4	17	US-10-378-089-1	Sequence 1, Appl
6	28	40.0	5	US-10-096-986-13	Sequence 13, Appl
7	28	40.0	8	US-10-182-252A-154	Sequence 154, App
8	28	40.0	9	US-10-264-309-397	Sequence 397, App
9	28	40.0	9	US-10-182-252A-142	Sequence 142, App
10	28	40.0	9	US-10-182-252A-273	Sequence 273, App
11	28	40.0	9	US-10-182-252A-796	Sequence 796, App
12	28	40.0	9	US-10-182-252A-840	Sequence 840, App
13	28	40.0	9	US-10-182-252A-1156	Sequence 1156, App

14	28	40.0	9	15	US-10-182-252A-1157	Sequence 1157, App
15	28	40.0	9	15	US-10-182-252A-1158	Sequence 1158, App
16	28	40.0	9	15	US-10-182-252A-1159	Sequence 1159, App
17	28	40.0	9	15	US-10-182-252A-1173	Sequence 1173, App
18	28	40.0	9	16	US-10-415-014-516	Sequence 516, App
19	28	40.0	9	16	US-10-415-014-624	Sequence 624, App
20	28	40.0	10	9	US-09-055-744-5	Sequence 5, Appl
21	28	40.0	10	16	US-10-415-014-572	Sequence 7, Appl
22	28	40.0	12	9	US-09-055-744-7	Sequence 2, Appl
23	28	40.0	14	14	US-10-148-936-2	Sequence 682, App
24	28	40.0	16	16	US-10-481-180-682	Sequence 19, Appl
25	28	40.0	18	9	US-09-880-713A-19	Sequence 9, Appl
26	28	40.0	18	9	US-09-226-248B-9	Sequence 1296, App
27	27	38.6	8	15	US-10-182-252A-1296	Sequence 140, App
28	27	38.6	9	15	US-10-182-252A-140	Sequence 272, App
29	27	38.6	9	15	US-10-182-252A-272	Sequence 884, App
30	27	38.6	9	15	US-10-182-252A-884	Sequence 885, App
31	27	38.6	9	15	US-10-182-252A-899	Sequence 899, App
32	27	38.6	9	15	US-10-182-252A-900	Sequence 900, App
33	27	38.6	9	15	US-10-182-252A-900	Sequence 51, Appl
34	27	38.6	10	14	US-10-283-349-51	Sequence 10, Appl
35	27	38.6	12	9	US-09-997-579-10	Sequence 6, Appl
36	27	38.6	12	14	US-10-360-522-6	Sequence 224, App
37	27	38.6	14	9	US-09-826-290-224	Sequence 3, Appl
38	27	38.6	14	14	US-10-162-134A-3	Sequence 47, Appl
39	27	38.6	14	15	US-10-264-309-47	Sequence 8, Appl
40	27	38.6	16	14	US-10-357-479-8	Sequence 753, App
41	27	38.6	17	14	US-10-225-567A-753	Sequence 752, App
42	27	38.6	18	14	US-10-225-567A-752	Sequence 8, Appl
43	27	38.6	19	9	US-09-997-579-8	Sequence 204, App
44	26.5	37.9	16	14	US-10-161-791-204	Sequence 4, Appl
45	26	37.1	8	9	US-09-055-744-4	

ALIGNMENTS

RESULT 1

US-10-334-726-111  
; Sequence 111, Application US/10334726  
; Publication No. US20030211521A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE  
; TITLE OF INVENTION: BREAST CANCER ANTIGEN  
; FILE REFERENCE: 1090-36  
; CURRENT APPLICATION NUMBER: US/10/334,726  
; CURRENT FILING DATE: 2003-01-02  
; PRIOR APPLICATION NUMBER: US/09/645,446  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00866  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: GB 9805877.9  
; PRIOR FILING DATE: 1998-09-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:predicted  
; OTHER INFORMATION: peptide  
; OTHER INFORMATION: peptide  
US-10-334-726-111

Query Match 50.0%; Score 35; DB 14; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 PVEKLLPL 11  
Db 1 PVEKLLPL 8

## RESULT 2

US-10-232-544-88  
; Sequence 88, Application US/10232544  
; Publication No. US20030199069A1  
; GENERAL INFORMATION:  
; APPLICANT: Fugisang, Claus  
; APPLICANT: Okkels, Jens  
; APPLICANT: Petersen, Dorte  
; APPLICANT: Pakkar, Shamkant  
; APPLICANT: Thellersen, Marianne  
; APPLICANT: Svenden, Allan  
; APPLICANT: Borch, Kim  
; APPLICANT: Royer, John  
; APPLICANT: Kretschmar, Titus  
; APPLICANT: Halkier, Torben  
; APPLICANT: Vind, Jesper  
; APPLICANT: Jorgensen, Steen  
; TITLE OF INVENTION: NO. US20030199069A1el Lipolytic Enzymes  
; FILE REFERENCE: 4455.404-US  
; CURRENT APPLICATION NUMBER: US/10/232,544  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/007,288  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 162  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide addition  
US-10-232-544-88

Query Match 47.1%; Score 33; DB 14; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12  
|||:||||  
Db 3 PPRPELLPIS 12

## RESULT 3

US-10-024-123-31  
; Sequence 31, Application US/10024123  
; Publication No. US20030022263A1  
; GENERAL INFORMATION:  
; APPLICANT: Kastan, Michael  
; APPLICANT: Canman, Christine  
; APPLICANT: Kim, Seong-Tae  
; APPLICANT: Lim, Dae-Sik  
; APPLICANT: St. Jude Children's Research Hospital  
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
; FILE REFERENCE: 2427/1F142  
; CURRENT APPLICATION NUMBER: US/10/024,123  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/400,653  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: 09/248,061  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-123-31

Query Match 42.9%; Score 30; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPVEKLLPLS 12  
|||:||||  
Db 4 PPVSQELPCS 13

## RESULT 4

US-10-072-602B-616  
; Sequence 616, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 616  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Conus flavidus  
US-10-072-602B-616

Query Match 41.4%; Score 29; DB 14; Length 15;  
Best Local Similarity 60.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPPVEKLLP 10  
|||||  
Db 4 SNPPCSYLNLP 13

## RESULT 5

US-10-378-089-1  
; Sequence 1, Application US/10378089  
; Publication No. US20040052780A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KAZUHISA  
; APPLICANT: KAWAMOTO, SEIJI  
; APPLICANT: GOTO, TAKESHI  
; APPLICANT: SATO, SHUJI  
; APPLICANT: GOTO, SIGERU  
; TITLE OF INVENTION: IMMUNOSUPPRESSANT  
; FILE REFERENCE: 7388/80237  
; CURRENT APPLICATION NUMBER: US/10/378,089  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: JP P2002-260681  
; PRIOR FILING DATE: 2002-09-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-378-089-1

Query Match 41.4%; Score 29; DB 15; Length 17;  
Best Local Similarity 55.6%; Pred. No. 7.5e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKLL 9  
| | | | : |  
Db 5 SGPPVSELI 13

## RESULT 6

US-10-096-986-13  
; Sequence 13, Application US/10096986  
; Publication No. US20030083464A1  
; GENERAL INFORMATION:

APPLICANT: Ferrari, Franco A.  
Richardson, Charles  
Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Criseman, John W.

TITLE OF INVENTION: No US20030083464A1 Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:

ADDRESSER: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/096,986

FILING DATE: 12-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/444,791

FILING DATE: 22-No. US20030083464A1-1999

APPLICATION NUMBER: US 08/482,085

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard P.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-096-986-13

Query Match 40.0%; Score 28; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7

| | | | |

Db 1 PPVEK 5

## RESULT 7

US-10-182-252A-154

; Sequence 154, Application US/10182252A

; Publication No. US20040072162A1

; GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

TITLE OF INVENTION: CONTROL OF HIV INFECTIONS

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

CURRENT FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 154

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-154

Query Match 40.0%; Score 28; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPPV 5

| | | | |

Db 2 SNPPV 6

## RESULT 8

US-10-264-309-397

; Sequence 397, Application US/10264309

; Publication No. US20040022794A1

; GENERAL INFORMATION:

APPLICANT: DURHAM, L. KATHRYN

APPLICANT: FRIEDMAN, DAVID L.

APPLICANT: HERATH, HERATH

APPLICANT: KIMMEL, LIDA H.

APPLICANT: PAREKH, RAJESH B.

APPLICANT: POTTER, DAVID M.

APPLICANT: ROHLFF, CHRISTIAN

APPLICANT: SILBER, B. MICHAEL

APPLICANT: SNYDER, PETER J.

APPLICANT: SOARES, HOLLY D.

APPLICANT: STIGER, THOMAS R.

APPLICANT: SUNDERLAND, P. TREY

APPLICANT: TOWNSEND, ROBERT R.

APPLICANT: WHITE, W. FROST

APPLICANT: WILLIAMS, STEPHEN A.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,

TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE

FILE REFERENCE: POA-002.01

CURRENT APPLICATION NUMBER: US/10/264,309

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: 60/326,708

PRIOR FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

SOFTWARE: PatentIn Version 2.1

SEQ ID NO 397

; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-309-397

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LPLSLK 14  
Db 4 LPLSLK 9  
|||||

RESULT 9  
US-10-182-252A-142  
; Sequence 142, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-142

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
Db 3 SNPPV 7  
|||||

RESULT 10  
US-10-182-252A-273  
; Sequence 273, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29

; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 273  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-273

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
Db 3 SNPPV 7  
|||||

RESULT 11  
US-10-182-252A-796  
; Sequence 796, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 796  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-796

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEKL 8  
Db 4 PPIERL 9  
|||:|

RESULT 12  
US-10-182-252A-840  
; Sequence 840, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE

```

; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 840
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-840
```

```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 PPVEKL 8
        ||:|:|
DB      4 PPIERL 9
```

```

RESULT 13
US-10-182-252A-1156
; Sequence 1156, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1156
```

```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SNPPV 5
        |||||
DB      3 SNPPV 7
```

```

RESULT 14
US-10-182-252A-1157
; Sequence 1157, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1157
```

```

Query Match      40.0%; Score 28; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 SNPPV 5
        |||||
DB      3 SNPPV 7
```

```

RESULT 15
US-10-182-252A-1158
; Sequence 1158, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-1158
```

Query Match 40.0%; Score 28; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPPV 5  
|  
|  
|  
|  
|  
Db 3 SNPPV 7

Search completed: October 27, 2004, 01:30:40  
Job time : 1034 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 21:31:56 ; Search time 1888 Seconds

(without alignments)  
350.665 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1863394

Minimum DB seq length: 0

Maximum DB seq length: 57

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool.p/US09980881/runat\_26102004\_083352\_5573/app.query.fasta\_1.199  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosu62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=57  
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	65.7	43	6 AX093019	AX093019 Sequence
C 2	37	52.9	41	6 AX519039	AX519039 Sequence
C 3	36	51.4	51	6 CQ001968	CQ001968 Sequence
4	35.5	50.7	39	6 A24246	A24246 Oligonucleo

C	5	35	50.0	45	6	CQ767550	Sequence
C	6	35	50.0	45	6	AX201424	Sequence
	7	34	48.6	34	6	AR364159	Sequence
	8	34	48.6	40	6	AR053703	Sequence
	9	34	48.6	40	6	AR258638	Sequence
C	10	34	48.6	40	6	AX107547	Sequence
C	11	34	48.6	41	6	AR036483	Sequence
C	12	34	48.6	41	6	AR069442	Sequence
C	13	34	48.6	41	6	I73464	Sequence
	14	34	48.6	48	6	BD243527	Nucleotid
	15	34	48.6	48	6	AX034950	Sequence
	16	34	48.6	51	6	AR077572	Sequence
	17	34	48.6	51	6	AR265635	Sequence
	18	33	47.1	36	6	AR088742	Sequence
	19	33	47.1	36	6	AR095469	Sequence
	20	33	47.1	36	6	AR112470	Sequence
	21	33	47.1	36	6	BD070735	Vectors h
	22	33	47.1	36	6	BD070761	Vectors h
C	23	33	47.1	41	6	AR036485	Sequence
C	24	33	47.1	41	6	AR069444	Sequence
C	25	33	47.1	41	6	I73466	Sequence
	26	33	47.1	44	6	BD091851	Novel cyt
	27	33	47.1	44	6	BD091885	Novel cyt
C	28	33	47.1	46	6	AI6157	Primer. 10/
C	29	33	47.1	48	9	HS3B3VB19	X84265 H.sapiens m
C	30	33	47.1	48	9	HSU14066	U14066 Human cell
C	31	33	47.1	48	9	HSU14068	U14068 Human cell
C	32	33	47.1	50	6	CQ002840	Sequence
C	33	33	47.1	51	6	CQ003669	Sequence
C	34	33	47.1	51	6	AX165250	Sequence
C	35	33	47.1	51	6	AX165250	Sequence
	36	32	45.7	20	6	AX379575	Sequence
C	37	32	45.7	23	6	AX587292	Sequence
	38	32	45.7	32	6	BD061431	Novel pol
	39	32	45.7	33	6	AR268900	Sequence
	40	32	45.7	33	6	AR492234	Sequence
C	41	32	45.7	39	10	S86280	TCR V beta
C	42	32	45.7	47	6	AR291010	Sequence
	43	32	45.7	51	6	CQ001695	Sequence
	44	32	45.7	51	6	AX162153	Sequence
	45	32	45.7	51	6	AX162154	Sequence

ALIGNMENTS

RESULT 1  
AX093019/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX093019  
Sequence 24 from Patent WO0118192.  
AX093019  
AX093019.1 GI:13509494

linear PAT 30-MAR-2001

synthetic construct  
synthetic construct  
artificial sequences.

1

Gruber V. and Comeau, D.

Synthetic vectors, transgenic plants containing them, and methods

for obtaining them

Patent: WO 0118192-A 24 15-MAR-2001;

MERISTEM THERAPEUTICS (FR)

Location/Qualifiers

1..43

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Oligo Desoxynucleotide containing StuI restriction

site"

ORIGIN

Alignment Scores:

Pred. No.: 9.58

Score: 46.00

Length:

Matches: 43

9

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Percent Similarity: 90.91%      Conservative: 1
Best Local Similarity: 81.82%    Mismatches: 1
Query Match: 65.71%             Indels: 0
DB: 6                           Gaps: 0

US-09-980-881A-9 (1-14) x AX093019 (1-43)

Qy 1 SerAsnProValGluLysLeuLeuProLeu 11
Db 38 TCGACCCCTCCGCGTGAAGGCGCTTCTACCATTA 6

RESULT 2
LOCUS AX519039 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5237 from Patent WO02052044.
ACCESSION AX519039
VERSION AX519039.1 GI:23569098
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5237 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 381 Length: 41
Score: 27.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 52.86% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX519039 (1-41)

Qy 3 ProProValGluLysLeuLeuProLeu 11
Db 33 CCACCTGTGGAGMCTTCTCTACCACTG 7

RESULT 3
LOCUS CQ001968 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 608 from Patent WO0147944.
ACCESSION CQ001968
VERSION CQ001968.1 GI:41008600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 608 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Accession number cg43927434"

ORIGIN
Percent Similarity: 90.91%      Conservative: 1
Best Local Similarity: 81.82%    Mismatches: 1
Query Match: 65.71%             Indels: 0
DB: 6                           Gaps: 0

US-09-980-881A-9 (1-14) x CQ001968 (1-51)

Qy 1 SerAsnProValGluLysLeuLeuProLeuSerLeu 13
Db 1 AGCAGGCGCTCTGTAGCTCGCTAATTACCGTGACTTTA 39

RESULT 4
LOCUS A24246 39 bp DNA linear PAT 04-DEC-1994
DEFINITION Oligonucleotide.
ACCESSION A24246
VERSION A24246.1 GI:833653
KEYWORDS Rattus rattus (black rat)
SOURCE Rattus rattus
ORGANISM Rattus rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS HUMANIZED INTERLEUKIN-2 RECEPTORS ANTIBODIES
TITLE Patent: WO 9301289-A 30 21-JAN-1993;
JOURNAL Location/Qualifiers
1..39
/organism="Rattus rattus"
/mol_type="unassigned DNA"
/db_xref="taxon:10117"

ORIGIN
Alignment Scores:
Pred. No.: 677 Length: 39
Score: 35.50 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 50.71% Indels: 1
DB: 6 Gaps: 1

US-09-980-881A-9 (1-14) x A24246 (1-39)

Qy 3 ProProValGluLysLeuLeuProLeuSerLeuLys 14
Db 5 CCCCCCGGTG---AAGCTGTACTCTTTCACAGAAA 37

RESULT 5
LOCUS CQ767550/c 45 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 17 from Patent EP1386931.
ACCESSION CQ767550
VERSION CQ767550.1 GI:45095665
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.
TITLE Human neurotrophin homologue
JOURNAL Patent: EP 1386931-A 17 04-FEB-2004;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..45
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

ORIGIN

```



Alignment Scores:  
 Pred. No.: 953 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CQ767550 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
 ||||| |||||::: |||||  
 DB 32 AGCAATGCCCGGTTCAAGCGCTGCTCCCC 3

RESULT 6  
 AX201424/c  
 LOCUS AX201424 45 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 103 from Patent WO0153486.  
 ACCESSION AX201424  
 VERSION AX201424.1 GI:15391230  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
 Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,  
 Stone, D.M., Watanabe, C.K. and Wood, W.I.  
 TITLE Compositions and methods for the treatment of tumour  
 JOURNAL Patent: WO 0153486-A 103 26-JUL-2001;  
 Genentech, Inc. (US)

FEATURES  
 source  
 1..45  
 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic Oligonucleotide Probe."

ORIGIN

Alignment Scores:  
 Pred. No.: 953 Length: 45  
 Score: 35.00 Matches: 7  
 Percent Similarity: 80.00% Conservative: 1  
 Best Local Similarity: 70.00% Mismatches: 2  
 Query Match: 50.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX201424 (1-45)

QY 1 SerAsnProValGluLysLeuLeuPro 10  
 ||||| |||||::: |||||  
 DB 32 AGCAATGCCCGGTTCAAGCGCTGCTCCCC 3

RESULT 7  
 AR364159  
 LOCUS AR364159 34 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 42 from patent US 5256545.  
 ACCESSION AR364159  
 VERSION AR364159.1 GI:34426485  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 34)  
 AUTHORS Brown, M.S., Goldstein, J.L., Russell, D.W. and Sudhof, T.C.  
 TITLE Sterol Regulatory Elements  
 JOURNAL Patent: US 5256545-A 42 26-OCT-1993;  
 FEATURES  
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 1..34  
 Location/Qualifiers  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.11e+03 Length: 34  
 Score: 34.00 Matches: 7  
 Percent Similarity: 70.00% Conservative: 0  
 Best Local Similarity: 70.00% Mismatches: 3  
 Query Match: 48.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR364159 (1-34)

QY 2 AsnProValGluLysLeuLeuProLeu 11  
 ||||| |||||::: |||||  
 DB 4 AATCACCCCACTGCAGAAACTCTCCCTCG 33

RESULT 8  
 AR053703  
 LOCUS AR053703 40 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 127 from patent US 5834252.  
 ACCESSION AR053703  
 VERSION AR053703.1 GI:5978565  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Stemmer, W. Peter, Christiaan, and Lipshutz, R.J.  
 TITLE End-complementary polymerase reaction  
 JOURNAL Patent: US 5834252-A 127 10-NOV-1998;  
 FEATURES  
 Location/Qualifiers  
 1..40  
 source  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.29e+03 Length: 40  
 Score: 34.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4  
 Best Local Similarity: 50.00% Mismatches: 1  
 Query Match: 48.57% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR053703 (1-40)

QY 3 ProProValGluLysLeuLeuProLeuSer 12  
 |||||::: |||||::: |||||  
 DB 3 CCGCCTTTGAGTGAGTGATACCGCTCGCC 32

RESULT 9  
 AR258638  
 LOCUS AR258638 40 bp DNA linear PAT 20-DEC-2002  
 DEFINITION Sequence 127 from patent US 6489146.  
 ACCESSION AR258638  
 VERSION AR258638.1 GI:27309014  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Stemmer, W.P.C. and Lipshutz, R.J.  
 TITLE End-complementary polymerase reaction  
 JOURNAL Patent: US 6489146-A 127 03-DEC-2002;  
 FEATURES  
 Location/Qualifiers  
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 source  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 1.29e+03 Length: 40  
 Score: 34.00 Matches: 5  
 Percent Similarity: 90.00% Conservative: 4

```

Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR258638 (1-40)

Qy 3 ProProValGluLysLeuLeuProLeuSer 12
Db 3 CGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 10
LOCUS AX107547 40 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 366 from Patent WO0123606.
ACCESSION AX107547
VERSION AX107547.1 GI:13923032
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Grabowski,R. and Berghof,K.
TITLE Nucleic acid molecules for detecting bacteria and phylogenetic
units of bacteria
JOURNAL Patent: WO 0123606-A 366 05-APR-2001;
Biotecon Diagnostics GmbH (DE)
FEATURES
source
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/organism="Bradyrhizobium japonicum"
/mol_type="unassigned DNA"
/db_xref="taxon:375"

ORIGIN
Alignment Scores:
Pred. No.: 1.29e+03 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AX107547 (1-40)

Qy 4 ProValGluLysLeuLeuProLeuSer 12
Db 40 CCAATCGAAGATTAGTACCGGTAGC 14

RESULT 11
LOCUS AR036483 41 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5872218.
ACCESSION AR036483
VERSION AR036483.1 GI:5953151
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Human platelet-derived growth factor receptor extracellular domain
antibodies
JOURNAL Patent: US 5872218-A 16 16-FEB-1999;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 55.56% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR069442 (1-41)

Qy 1 SerAsnProProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 12
LOCUS AR069442 41 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 16 from patent US 5891652.
ACCESSION AR069442
VERSION AR069442.1 GI:7220330
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Methods of using domains of extracellular region of human
platelet-derived growth factor receptor polypeptides
JOURNAL Patent: US 5891652-A 16 06-APR-1999;
FEATURES
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x AR036483 (1-41)

Qy 1 SerAsnProProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAACCTT 14

RESULT 13
LOCUS I73464 41 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 16 from patent US 5686572.
ACCESSION I73464
VERSION I73464.1 GI:3009605
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
TITLE Domains of extracellular region of human platelet derived growth
factor receptor polypeptides
JOURNAL Patent: US 5686572-A 16 11-NOV-1997;
FEATURES
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.32e+03 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2

```

Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 48.57% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x I73464 (1-41)

QY 1 SerAsnProProValGluLysLeu 8  
DB 37 TCGATCCGCCAGTTAAGCACTT 14

## RESULT 14

BD243527

LOCUS

DEFINITION BD243527 48 bp DNA linear PAT 17-JUL-2003  
Nucleotide fragment, probe, primer, reagent, and method for  
detecting nucleotide sequence derived from replication origin of  
pBR322.

## ACCESSION

BD243527

VERSION BD243527.1 GI:33053297

## KEYWORDS

JP 2002537856-A/34.

## SOURCE

unidentified

## ORGANISM

unclassified.

## REFERENCE

1 (bases 1 to 48)

## AUTHORS

Lamy, D.

## TITLE

Nucleotide fragment, probe, primer, reagent, and method for  
detecting nucleotide sequence derived from replication origin of  
Patent: JP 2002537856-A 34 12-NOV-2002;

## JOURNAL

TRANSGENE

OS PBR322 plasmid

PN JP 2002537856-A/34

PD 12-NOV-2002

PF 03-MAR-2000 JP 2000603424

PR 05-MAR-1999 FR 99/02968

PI DIDIER LAMY

PC C12N15/09,C12Q1/68,C12N15/00

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

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CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

CC Nucleotide fragment, probe, primer, reagent, and method for

## AUTHORS

TITLE

Nucleotide fragment, probe, primer, reagent and method for  
detecting a nucleotide sequence derived from pBR322 replication  
origin

## JOURNAL

Patent: WO 0053803-A 34 14-SEP-2000;

## FEATURES

LAMY DIDIER (FR) ; TRANSGENE (FR)

## source

Location/Qualifiers

1..48

/organism="Cloning vector pBR322"

/mol\_type="unassigned DNA"

/db\_xref="taxon:47470"

## ORIGIN

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Length: 48

Matches: 5

Conservative: 4

Mismatches: 1

Indels: 0

Gaps: 0

Percent Similarity: 50.00%

Best Local Similarity: 48.57%

Query Match: 6

DB: 19

US-09-980-881A-9 (1-14) x AX034950 (1-48)

QY 3 ProProValGluLysLeuProLeuSer 12

DB 19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48

Search completed: October 26, 2004, 22:56:44

Job time : 1895 secs

## FEATURES

source

Location/Qualifiers

1..48

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32844"

## ORIGIN

Alignment Scores:

Pred. No.: 1.53e+03

Score: 34.00

Length: 48

Matches: 5

Conservative: 4

Mismatches: 1

Indels: 0

Gaps: 0

Percent Similarity: 50.00%

Best Local Similarity: 48.57%

Query Match: 6

DB: 19

US-09-980-881A-9 (1-14) x BD243527 (1-48)

QY 3 ProProValGluLysLeuProLeuSer 12

DB 19 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 48

RESULT 15

AX034950

LOCUS

DEFINITION AX034950 48 bp DNA linear PAT 15-NOV-2000

Sequence 34 from Patent WO0053803.

ACCESSION AX034950

VERSION AX034950.1 GI:11190875

KEYWORDS

Cloning vector pBR322

SOURCE

Cloning vector pBR322

ORGANISM

artificial sequences; vectors.

REFERENCE

1



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 21:18:21 ; Search time 389 Seconds  
(without alignments)  
188.925 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 4074946

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool\_p/US09980881/runat\_26102004\_083352\_5565/app\_query.fasta\_1.199  
-DB=N Geneseq 23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57  
-USER=US09980881 @CGN 1.1.708 @runat\_26102004\_083352\_5565 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: Geneseqn1990s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002as:.\*  
7: Geneseqn2002bs:.\*  
8: Geneseqn2003as:.\*  
9: Geneseqn2003bs:.\*  
10: Geneseqn2003cs:.\*  
11: Geneseqn2003ds:.\*  
12: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	46	65.7	43	4 AAF80298	Aaf80298 PCR prime
C 2	37	52.9	41	6 ABZ48454	Abz48454 Human org
C 3	51	52.9	51	2 AAT00624	Aat00624 Human (2'
C 4	36	51.4	36	10 ADD69569	Add69569 Food enri
C 5	36	51.4	36	10 ADD69568	Add69568 Food enri
C 6	36	51.4	51	4 AAL27400	Aal27400 Human SNP

C 7	35.5	50.7	39	2 AAO36595	Aao36595 PCR prime
C 8	35	50.0	45	2 AAZ33905	Aaz33905 Human PRO
C 9	35	50.0	45	3 AAC78611	Aac78611 Human PRO
C 10	35	50.0	45	6 ABK40321	Abk40321 Oligonuc1
C 11	35	50.0	45	8 ACA63473	Aca63473 Novel hum
C 12	35	50.0	45	8 ACA71637	Aca71637 Human PRO
C 13	35	50.0	45	8 ABX92277	Abx92277 Human PRO
C 14	35	50.0	45	8 ACA66018	Acx66018 Human sec
C 15	35	50.0	45	9 ADA24556	Ada24556 Secreted
C 16	35	50.0	45	9 ACD29619	Acd29619 Novel hum
C 17	35	50.0	45	9 ADA12217	Ada12217 Human sec
C 18	35	50.0	45	9 ACD29034	Acd29034 Novel hum
C 19	35	50.0	45	10 ADB73523	Adb73523 Human PRO
C 20	35	50.0	45	10 ADB76239	Adb76239 Human PRO
C 21	35	50.0	45	10 ADC43665	Adc43665 Human PRO
C 22	35	50.0	45	10 ADC61425	Adc61425 Human PRO
C 23	35	50.0	45	10 ADC63389	Adc63389 Human PRO
C 24	35	50.0	45	10 ADC66489	Adc66489 Human PRO
C 25	35	50.0	45	10 ADC68613	Adc68613 Human PRO
C 26	35	50.0	45	10 ADC62673	Adc62673 Human PRO
C 27	35	50.0	45	10 ADC67738	Adc67738 Human PRO
C 28	35	50.0	45	10 ADC41058	Adc41058 Human PRO
C 29	35	50.0	45	10 ADC67113	Adc67113 Human PRO
C 30	35	50.0	45	10 ADC62049	Adc62049 Human PRO
C 31	35	50.0	45	10 ADC41682	Adc41682 Human PRO
C 32	35	50.0	45	10 ADE49051	Ade49051 Human PRO
C 33	35	50.0	45	10 ADE35105	Ade35105 Human PRO
C 34	35	50.0	45	10 ADE16219	Ade16219 Human PRO
C 35	35	50.0	45	10 ADD72834	Add72834 Human PRO
C 36	35	50.0	45	10 ADD72192	Add72192 Human PRO
C 37	35	50.0	45	10 ADE16843	Ade16843 Human PRO
C 38	35	50.0	45	10 ADF46857	Adf46857 Human PRO
C 39	35	50.0	45	10 ADG52614	Adg52614 Human PRO
C 40	35	50.0	45	10 ADG59934	Adg59934 Human PRO
C 41	35	50.0	45	10 ADI60694	Adi60694 Tumour th
C 42	35	50.0	45	10 ADJ37384	Adj37384 Novel hum
C 43	35	50.0	45	10 ACD42438	Acd42438 Novel hum
C 44	35	50.0	45	12 ADE48351	Ade48351 Human PRO
C 45	35	50.0	45	12 ADE89452	Ade89452 Human PRO

ALIGNMENTS

RESULT 1

AAF80298/c  
ID AAF80298 standard; DNA; 43 BP.  
XX  
AC AAF80298;  
XX  
DT 29-JUN-2001 (first entry)  
XX  
DE PCR primer used to amplify the RK2 origin of replication.  
XX  
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant;  
KW PCR primer; ss.  
XX  
OS Escherichia coli.  
PN FR2798139-A1.  
XX  
PD 09-MAR-2001.  
XX  
PF 03-SEP-1999; 99FR-00011112.  
XX  
PR 03-SEP-1999; 99FR-00011112.  
XX  
(MERI-) MERISTEM THERAPEUTICS SA.  
PA  
XX  
PI Gruber V, Comeau D;  
XX  
DR WPI; 2001-259847/27.  
XX

PT New vector free from non-essential elements, useful for transforming  
 PT cells for protein production and for preparing transgenic plants.  
 XX  
 PS Example 1; Page 13; 180pp; French.  
 XX  
 CC The specification describes a synthetic vector containing only those  
 CC elements essential for its functionality and transgenesis of a cell  
 CC (especially a plant cell). The vector consists of at most one origin of  
 CC replication (ori), at most one sequence encoding a selection agent and a  
 CC trfA locus encoding a protein that increases the level of plasmid  
 CC replication. The vector particularly contains an RK2 ori, especially oriV  
 CC from pRK2 of *Escherichia coli* with a broad host range, an antibiotic  
 CC resistance gene (especially nptII conferring resistance to kanamycin in  
 CC bacteria) and a trfA locus from pRK2 encoding the proteins p285 and p382.  
 CC The vectors are used to prepare transgenic plants and transformed host  
 CC cells for production of a heterologous proteins, e.g. insulin,  
 CC interferon, lipase, blood proteins and anti-inflammatory agents. PCR  
 CC primers AAF80297-98 were used to amplify the RK2 ori, and the amplified  
 CC fragment was used to construct plasmids of the invention  
 XX  
 SQ Sequence 43 BP; 11 A; 6 C; 17 G; 9 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.67 Length: 43  
 Score: 46.00 Matches: 9  
 Percent Similarity: 90.91% Conservative: 1  
 Best Local Similarity: 81.82% Mismatches: 1  
 Query Match: 65.71% Indels: 0  
 DB: 4 Gaps: 0

US-09-980-881A-9 (1-14) x AAF80298 (1-43)

Qy 1 SerAenProValGluLeuLeuProLeu 11  
 |||||  
 Db 38 TCGAACCTCCGCGAAGGCTTCTACCATTA 6

RESULT 2

ABZ48454/c

ID ABZ48454 standard; DNA; 41 BP.

XX AC ABZ48454;

XX DT 26-JUN-2003 (first entry)

XX DE Human organic cation transporter OCT1 gene polymorphic site, #5237.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
 KW drug evaluation; drug screening; genotyping; genetic profiling;  
 KW therapeutic customisation; adverse reaction; clinical trial;  
 KW drug approval; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT variation

XX FT /\*tag= a

XX FT /standard\_name= "single nucleotide polymorphism (SNP) "

XX PN WO200252044-A2.

XX PD 04-JUL-2002.

XX PF 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-00399443.

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

XX XX (RIKE ) RIKEN KK.

XX FI Nakamura Y, Sekine A, Iida A, Saito S;

XX XX WPI; 2002-583571/62.

DR

XX

PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PS detecting at least one polymorphism in the drug metabolizing enzyme  
 XX nucleic acid.

PS Claim 23; Page 166; 2785pp; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX  
 SQ Sequence 41 BP; 11 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 276 Length: 41  
 Score: 37.00 Matches: 7  
 Percent Similarity: 77.78% Conservative: 0  
 Best Local Similarity: 77.78% Mismatches: 2  
 Query Match: 52.86% Indels: 0  
 DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x ABZ48454 (1-41)

Qy 3 ProProValGluLeuLeuProLeu 11

|||||  
 Db 33 CCACCTGTGGAGCCTTCTTCCATCCTG 7

RESULT 3

AAT00624

ID AAT00624 standard; DNA; 51 BP.

XX AC AAT00624;

XX XX

DT 03-FEB-1996 (first entry)

XX DE Human (2'-5') oligo A synthetase antigenic peptide CDNA.

XX KW (2'-5') oligo A synthetase; interferon; antigenic peptide; ss.

XX OS Homo sapiens.

XX XX CA1337281-C.

PN



CC more by weight of gamma-glutamyl cysteine based on dry cells in the  
 CC logarithmic growth phase when cultured in the minimum medium, adding the  
 CC obtained culture, optionally after heating, to a food or drink material  
 CC and processing. The yeast of the invention may be used for producing food  
 CC and drink with enriched gamma-glutamyl cysteine or cysteine which is  
 CC useful in food industry e.g. for seasoning. In this way, food and drink  
 CC can be cheaply produced with improved flavour. The current sequence is  
 CC that of the food enrichment-related PCR primer of the invention.

XX SQ Sequence 36 BP; 7 A; 4 C; 9 G; 16 T; 0 U; 0 Other;

Alignment Scores: 352 Length: 36  
 Pred. No.: 36.00 Matches: 7  
 Score: 72.73% Conservative: 1  
 Percent Similarity: 63.64% Mismatches: 3  
 Best Local Similarity: 51.43% Indels: 0  
 Query Match: 10 Gaps: 0  
 DB:

US-09-980-881A-9 (1-14) x ADD69568 (1-36)

QY 4 ProValGluLysLeuLeuProLeuSerLeuLys 14

DB 33 CCTATTGAAATAATTACTACCCACCCAGAAAG 1

RESULT 6

AAL27400

ID AAL27400 standard; DNA; 51 BP.

XX AC AAL27400;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #608.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiopeptide; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.

XX PR 28-DEC-1999; 98US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.

XX PS Claim 1; Page 1561; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiopeptide,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
 CC protein coupled receptors and thioesterases. The present sequence is one

CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of the proteins listed above.  
 CC Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms

XX SQ Sequence 51 BP; 11 A; 18 C; 9 G; 13 T; 0 U; 0 Other;

Alignment Scores: 525 Length: 51  
 Pred. No.: 36.00 Matches: 7  
 Score: 76.92% Conservative: 3  
 Percent Similarity: 53.85% Mismatches: 3  
 Best Local Similarity: 51.43% Indels: 0  
 Query Match: 4 Gaps: 0  
 DB:

US-09-980-881A-9 (1-14) x AAL27400 (1-51)

QY 1 SerAsnProProValGluLysLeuLeuProLeuSerLeu 13

DB 1 AGCAGGCCTCTGTAGCTCGCTAATTACCCGTGACTTAA 39

RESULT 7

AAQ36595

ID AAQ36595 standard; DNA; 39 BP.

XX AC AAQ36595;

XX DT 25-MAR-2003 (revised)

XX DT 28-MAY-1993 (first entry)

XX PCR primer FH for construction of humanised Heavy chain anti IL-2 Ab.  
 DE antibody; monoclonal; chimaeric; grafted; humanised; IL-2; interleukin-2;  
 KW cytokines; interleukin-2 receptor; 55kD beta chain; activated T cells;  
 KW T cell mediated disease; graft versus host disease; transplant rejection;  
 KW autoimmune diseases; chemotherapy; immunosuppressants; T cell typing;  
 KW diagnosis; testing; detection; ss.

XX OS Synthetic.

XX PN WO9301289-A1.

XX PD 21-JAN-1993.

XX PF 10-JUL-1992; 92WO-GB001258.

XX PR 11-JUL-1991; 91GB-00015010.

XX PA (WELL) WELLCOME FOUND LTD.

XX PA (WALD) WALDMANN H.

XX PI Waldmann H, Winter GP, Crowe JS, Lewis AP;

XX WPI; 1993-045493/05.

XX Human interleukin-2 receptor antibodies - useful for treating and  
 PT preventing T-cell mediated diseases e.g. graft versus host disease,  
 PT transplant rejection etc.

XX PS Example; Page 42; 48pp; English.

XX This PCR primer was used with AAQ36594 in the construction of a humanised  
 CC anti-IL-2 antibody. The initial template for the reaction was anti-CD4  
 CC heavy chain (on KOL framework; WO9205274). (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX SQ Sequence 39 BP; 11 A; 12 C; 8 G; 8 T; 0 U; 0 Other;



Alignment Scores: 39  
Pred. No.: 469 Length: 39  
Score: 35.50 Matches: 9  
Percent Similarity: 83.33% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 50.71% Indels: 1  
DB: 2 Gaps: 1

US-09-980-881A-9 (1-14) x AAQ36595 (1-39)

QY 3 ProProValGluLysLeuLeuProLeuSerLeuLys 14

Db 5 CCCCCGGTG--AAGTGTACTCTTGACAGAAA 37

RESULT 8

AAZ33905/c

ID AAZ33905 standard; DNA; 45 BP.

XX AAZ33905;

XX 07-DEC-1999 (first entry)

XX Human PRO274 hybridisation probe.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 23-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 31-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080332P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 08-APR-1998; 98US-0081071P.

PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082766P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 30-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084411P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086192P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

(GETH ) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

XX New secreted and transmembrane polypeptides and their polynucleotides,  
XX useful for treating blood coagulation disorders, cancers and cellular  
XX adhesion disorders.

XX Example 4; Page 184; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
XX and their polynucleotides. The nucleotide sequences are useful as sources  
XX of probes, primers, for chromosome mapping, and for generation of  
XX antisense sequences. They can also be used to create transgenic animals.  
XX The proteins can be used to treat a variety of diseases and disorders,  
XX depending on their function. Diseases that may be treated include blood  
XX coagulation disorders, cancers and cellular adhesion disorders. They may

CC also be used to raise antibodies. AAC233891 to AAC234338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention

SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x AAC233905 (1-45)

Qy 1 SerAsnProProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 9

AAC78611/c

ID AAC78611 standard; DNA; 45 BP.

XX AAC78611;

XX 08-FEB-2001 (first entry)

DE Human PRO274 hybridisation probe SEQ ID NO:17.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
KW expressed sequence tag; detection; cancer; PCR primer; probe; ss.

OS Homo sapiens.

PN WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US004341.

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0145698P.

PR 29-OCT-1999; 99US-0162508P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US028565.

PR 30-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;

DR WPI; 2000-611443/58.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to  
PT target bioactive molecules to specific cells, and to modulate cellular  
PT activities.

XX Example 4; Page 235; 636pp; English.  
PS  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
CC polynucleotides and polypeptides can be used for detecting the presence  
CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
CC and for modulating biological activities of cells, using the polypeptides  
CC for specific targeting. The polypeptide targeting can be used to kill the  
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
CC AAC78987 represent PCR primers and probes used in the isolation of the  
CC PRO polynucleotide sequences  
XX  
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x AAC78611 (1-45)

Qy 1 SerAsnProProValGluLysLeuLeuPro 10

Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 10

ABK40321/c

ID ABK40321 standard; DNA; 45 BP.

XX ABK40321;

DT 15-JUL-2002 (first entry)

DE Oligonucleotide probe for human PRO274 DNA.

KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
KW neuroprotective; probe; ss.

OS Homo sapiens.

PN WO200153486-A1.

PD 26-JUL-2001.

XX 11-FEB-2000; 2000WO-US003565.

XX 08-MAR-1999; 99WO-US005028.

PR 11-MAR-1999; 99US-0123972P.

PR 11-MAY-1999; 99US-0133459P.

PR 02-JUN-1999; 99WO-US012252.

PR 22-JUN-1999; 99US-0140650P.

PR 22-JUN-1999; 99US-0140653P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 17-AUG-1999; 99US-0149395P.

PR 31-AUG-1999; 99US-0151689P.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021090.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH ) GENENTECH INC.

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XX AShtenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Example 10; Page 120; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC antibodies are useful for treating benign or malignant tumours (e.g.
CC renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC malignancies, other disorders such as neuronal, glial, astrocytal,
CC hypothalamic, glandular, macrophagal, stromal and blastocoeleic disorders,
CC inflammatory, immune and angiogenic disorders. The polynucleotide
CC sequences are also useful in gene therapy. The present invention
CC represents a probe used in the methods of the present invention
XX
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 672 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x ABK40321 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGCCCTGCTCCCC 3

RESULT 11
ACA63473/c
ID ACA63473 standard; DNA; 45 BP.
XX
XX ACA63473;
XX
XX 16-JUN-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein related probe #2.
XX
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; probe; ss.
XX
XX Homo sapiens.
XX
XX US2002192706-A1.
XX
XX 19-DEC-2002.
XX
XX 24-OCT-2001; 2001US-0099832.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX
11-MAR-1998; 98US-0077649P.
12-MAR-1998; 98US-0077791P.
13-MAR-1998; 98US-0078004P.
17-MAR-1998; 98US-00040220.
20-MAR-1998; 98US-0078886P.
20-MAR-1998; 98US-0078910P.
20-MAR-1998; 98US-0078936P.
20-MAR-1998; 98US-0078939P.
25-MAR-1998; 98US-0079294P.
26-MAR-1998; 98US-0079656P.
27-MAR-1998; 98US-0079663P.
27-MAR-1998; 98US-0079664P.
27-MAR-1998; 98US-0079689P.
27-MAR-1998; 98US-0079728P.
27-MAR-1998; 98US-0079786P.
30-MAR-1998; 98US-0079920P.
30-MAR-1998; 98US-0079923P.
31-MAR-1998; 98US-0080105P.
31-MAR-1998; 98US-0080107P.
31-MAR-1998; 98US-0080165P.
31-MAR-1998; 98US-0080194P.
01-APR-1998; 98US-0080327P.
01-APR-1998; 98US-0080328P.
01-APR-1998; 98US-0080333P.
01-APR-1998; 98US-0080334P.
08-APR-1998; 98US-0081049P.
08-APR-1998; 98US-0081070P.
08-APR-1998; 98US-0081071P.
09-APR-1998; 98US-0081195P.
09-APR-1998; 98US-0081203P.
09-APR-1998; 98US-0081229P.
15-APR-1998; 98US-0081817P.
15-APR-1998; 98US-0081819P.
15-APR-1998; 98US-0081838P.
15-APR-1998; 98US-0081952P.
15-APR-1998; 98US-0081953P.
21-APR-1998; 98US-0082568P.
21-APR-1998; 98US-0082569P.
22-APR-1998; 98US-0082700P.
22-APR-1998; 98US-0082704P.
22-APR-1998; 98US-0082797P.
22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082796P.
07-OCT-1998; 98WO-US021141.
20-NOV-1998; 98WO-US024855.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
10-MAR-1999; 99WO-US005190.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
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PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021086.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-328860/31.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
XX as PRO, useful for treating inflammation, organ failure, atherosclerosis,
XX cardiac injury, infertility, birth defects, premature aging, AIDS, or
XX cancer.
XX
XX Example 4; Page 125; 453pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
XX is at least 80 % sequence identity to, or the full-length coding sequence
XX of, any of 118 300-2100 nucleotide sequences, which encodes its
XX corresponding PRO polypeptide selected from 118 100-700 amino acid
XX sequences, all given in the specification. The nucleic acids and
XX polypeptides are useful for treating inflammatory diseases, organ
XX failure, atherosclerosis, cardiac injury, infertility, birth defects,
XX premature aging, AIDS, cancer, or diabetic complications. The nucleic
XX acids are useful as hybridisation probes, in chromosome and gene mapping,
XX and in generating antisense RNA or DNA. The polypeptides are useful as
XX pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
XX in tissue typing. This sequence represents a novel human secreted and
XX transmembrane PRO polypeptide associated probe
XX
XX Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 672 Length: 45
XX Score: 35.00 Matches: 7
XX Percent Similarity: 80.00% Conservative: 1
XX Best Local Similarity: 70.00% Mismatches: 2
XX Query Match: 50.00% Indels: 0
XX DB: 8 Gaps: 0
XX
XX US-09-980-881A-9 (1-14) x ACA63473 (1-45)
XX
XX QY 1 SerAnProValGluLysLeuPro 10
XX ||||| ||||| ||||| ||||| |||||
XX Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3
XX
XX RESULT 12
XX ACA71637/c
XX ID ACA71637 standard; DNA; 45 BP.
XX
XX AC ACA71637;
XX
XX DT 11-AUG-2003 (first entry)
XX
XX Human PRO polypeptide associated oligonucleotide SEQ ID NO 17.
XX
XX Human; ds; thrombolytic agent; interferon; interleukin; cytokine;
XX erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
XX apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
XX inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
XX gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
XX hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
XX glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;

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KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX Homo sapiens.
XX
XX US2002177553-A1.
XX
XX 28-NOV-2002.
XX
XX
XX 15-OCT-2001; 2001US-00978192.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 26-JUN-1998; 98US-00105413.
XX 07-OCT-1998; 98US-00168978.
XX 07-OCT-1998; 98WO-US021141.
XX 02-NOV-1998; 98US-00184216.
XX 06-NOV-1998; 98US-00187368.
XX 20-NOV-1998; 98WO-US024855.
XX 07-DEC-1998; 98US-00202054.
XX 22-DEC-1998; 98US-00218517.
XX 05-JAN-1999; 99WO-US000106.
XX 05-MAR-1999; 99US-00254465.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-00265686.
XX 10-MAR-1999; 99WO-US0005190.
XX 12-MAR-1999; 99US-00267213.
XX 12-APR-1999; 99US-00284291.
XX 14-MAY-1999; 99US-00311832.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 25-AUG-1999; 99US-00380137.
XX 25-AUG-1999; 99US-00380138.
XX 25-AUG-1999; 99US-00380142.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000WO-US006319.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.

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PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000US-00709238.  
PR 27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 22-MAR-2001; 2001WO-US009552.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Aashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
XX WPI; 2003-328499/31.  
XX  
XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as  
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying  
PT modulators of receptor-ligand interactions.  
XX  
XX Disclosure; SEQ ID NO 17; 55pp; English.  
XX  
XX The invention relates to an isolated secreted and transmembrane  
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful  
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for  
CC linking a bioactive molecule to a cell. The PRO polypeptide or an  
CC antibody against it is useful for modulating a biological activity of a  
CC cell. The PRO polypeptide is useful in industrial applications including  
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO  
CC polypeptide is also useful as a thrombolytic agent, interferon,  
CC interleukin, erythropoietin, colony stimulating factor and other  
CC cytokines. The PRO polypeptide is useful for treating disease such as  
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,  
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,  
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,  
CC Parkinson's disease; cardiovascular disease e.g. hypertension and  
CC myocardial ischaemia; kidney disease e.g. renal failure and  
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial  
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory  
CC bowel disease; reproductive disorders e.g. premature labour and  
CC preeclampsia; carcinogenesis. The present sequence represents a PRO  
CC polypeptide associated oligonucleotide of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?docID=20020177553  
XX  
XX  
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1

Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 8 Gaps: 0  
US-09-980-881A-9 (1-14) x ACA71637 (1-45)  
QY 1 SerAenProValGluLysLeuLeuPro 10  
DB 32 AGCAATGCCCGGTTCAAGGCGTGTCTCCC 3  
RESULT 13  
ABX92277/c  
ID ABX92277 standard; DNA; 45 BP.  
XX  
AC ABX92277;  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE Human PRO DNA probe SEQ ID No 17.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
KW cardiac insufficiency; nervous system disorder; kidney disorder;  
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
KW genetic disorder; cytostatic; antidiabetic; anti-inflammatory;  
KW antarthritic; anti-tumour; vulnery; antianaemic; dermatological;  
KW cardiant; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX US2002169284-A1.  
PN  
XX 14-NOV-2002.  
PD  
XX 16-OCT-2001; 2001US-00978697.  
PF  
XX 26-MAY-1981; 81US-00267213.  
PR  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0068364P.  
PR 10-NOV-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 12-MAR-1998; 98US-0077649P.  
PR 13-MAR-1998; 98US-0077791P.  
PR 17-MAR-1998; 98US-0078004P.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 26-JUN-1998; 98US-00105413.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98WO-US021141.  
PR 02-NOV-1998; 98US-00184216.  
PR 06-NOV-1998; 98US-00187368.  
PR 20-NOV-1998; 98WO-US024855.  
PR 07-DEC-1998; 98US-00202054.  
PR 22-DEC-1998; 98US-00218517.  
PR 05-JAN-1999; 99WO-US000106.  
PR 05-MAR-1999; 99US-00254465.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-00265686.

PR 10-MAR-1999; 99WO-US005190.  
PR 12-APR-1999; 99US-00284231.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US003376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000US-00709238.  
PR 27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 22-MAR-2001; 2001WO-US009552.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX (GETH ) GENENTECH INC.  
PA  
XX Ashkenazi A, Baker KP, Botstein D, Deenoyers L, Eaton D;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX WPI, 2003-288163/28.  
XX Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating cancer, kidney diseases, bone,  
PT cartilage disorders and immune deficiencies.  
XX  
XX Example 4; Page 126; 459pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating

CC biological activities of cells expressing PRO polypeptides, and for for  
CC identifying agonists or antagonists. The bioactive molecule maybe a  
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.  
CC The PRO polypeptides are useful for treating immune disorders, diabetes  
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system  
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,  
CC tumours, and wound healing. The polynucleotide sequences encoding PRO  
CC polypeptides are useful as hybridisation probes, in chromosome and gene  
CC mapping, in the generation of antisense RNA and DNA, in the preparation  
CC of PRO polypeptides, for generating transgenic animals or knockout  
CC animals, for the genetic analysis of individuals with genetic disorders,  
CC and in gene therapy. The present sequence represents a probe used in the  
CC examples of the present invention. Note: The sequence data for this  
CC patent was obtained in electronic format directly from the USPTO web site  
CC at seqdata.uspto.gov/psipdIDentry.html  
XX  
SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 672 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 8 Gaps: 0  
  
US-09-980-881A-9 (1-14) x ABX92277 (1-45)  
  
QY 1 SerAsnProProValGluLysLeuLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGGCGCTGCTCCC 3  
  
RESULT 14  
ACA66018/c  
ID ACA66018 standard; DNA; 45 BP.  
XX  
AC ACA66018;  
XX  
DT 24-JUN-2003 (first entry)  
DE Human secreted/transmembrane protein PRO274 probe.  
XX  
KW Human; ss; secreted protein; transmembrane protein; PRO; probe;  
KW malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;  
KW leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;  
KW infertility; premature aging; psoriasis; inflammatory disease;  
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;  
KW hepatitis; multiple sclerosis; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN US2003004102-A1.  
XX  
PD 02-JAN-2003.  
XX  
PF 15-OCT-2001; 2001US-00978189.  
XX  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.

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PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-0016897P.
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PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-00000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-00050528.
PR 10-MAR-1999; 99US-00265686.
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PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00310733.
PR 02-JUN-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-00283113.
PR 02-DEC-1999; 99US-0028551.
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PR 16-DEC-1999; 99US-0030095.
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PR 30-DEC-1999; 99US-0031274.
PR 05-JAN-2000; 2000US-0000219.
PR 05-JAN-2000; 2000US-0000277.
PR 05-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005004.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
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PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014941.
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PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
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PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-0030873.
PR 01-DEC-2000; 2000US-00723749.
PR 20-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
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PR 01-JUN-2001; 2001US-0017800.
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PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.

PR 30-JUL-2001; 2001US-00918585.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-341189/32.
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX Example 4; Page 121; 460pp; English.
XX The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence is a probe used in the isolation of a cDNA
CC encoding a PRO polypeptide
XX SQ Sequence 45 BP; 8 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 672 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 8 Gaps: 0

US-09-980-881A-9 (1-14) x ACA66018 (1-45)
QY 1 SerAsnProValGluLysLeuLeuPro 10
| | | | | | | | | | | | | | | | | | | |
Db 32 AGCAATGCCCGGTTCACAGCCTGCTCCCC 3

RESULT 15
ADA24556/C
ID ADA24556 standard; DNA; 45 BP.
XX
AC ADA24556;

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XX 20-NOV-2003 (first entry)  
XX Secreted and transmembrane PRO protein associated probe #2.  
XX Human; secreted and transmembrane protein; PRO: tissue typing;  
KW chromosome identification; vaccine; cancer; retinal disorder;  
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;  
KW wound healing; obesity; diabetes; hearing loss;  
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;  
KW haemoglobin associated disorder; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX US2003050241-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 16-OCT-2001; 2001US-00978564.  
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XX 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
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PR 21-NOV-1997; 97US-0065364P.  
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PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
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PR 20-NOV-1998; 98US-0109304P.  
PR 20-NOV-1998; 98WO-US024855.  
PR 22-DEC-1998; 98US-0113296P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 12-MAR-1999; 99US-0123957P.  
PR 29-MAR-1999; 99US-0126773P.  
PR 21-APR-1999; 99US-0130232P.  
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PR 28-APR-1999; 99US-0131445P.  
PR 14-MAY-1999; 99WO-US0134287P.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
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PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 30-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.



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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
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PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrari N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
XX
XX
XX
XX New isolated PRO polypeptides for example extracellular, secreted and
XX membrane bound proteins, useful for modulating the biological activities
XX of cells and for treating, for example diabetes, cancer, rheumatoid
XX arthritis, and hearing loss.
XX
XX Example 4; Page 132; 461pp; English.
XX
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
XX polypeptide (1). PRO337 polypeptide is useful for detecting PRO4993
XX polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
XX useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
XX useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
XX useful for linking a bioactive molecule to a cell expressing a PRO337
XX polypeptide, and PRO337 is useful for linking a bioactive molecule to a
XX cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
XX bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
XX polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for
XX
XX
XX Alignment Scores:
XX Pred. No.: 672 Length: 45
XX Score: 35.00 Matches: 7
XX Percent Similarity: 80.00% Conservative: 1
XX Best Local Similarity: 70.00% Mismatches: 2
XX Query Watch: 9 Indels: 0
XX DB: Gaps: 0
XX
XX US-09-980-881A-9 (1-14) x ADA24556 (1-45)
XX
XX Qy 1 SerAsnProProValGluLysLeuLeuPro 10
XX Db 32 AGCAATGCCCGGTTCGAAGCGTCTGCTCCC 3

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 26, 2004, 22:18:45 ; Search time 83 Seconds  
(without alignments)  
119.892 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVKLLPLSLK 14

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 934402

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO/spool\_p/US0980881/runat\_26102004\_083353\_5603/app\_query.fasta\_1.199  
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=57  
-USER=US0980881@cgn\_1\_105 @runat\_26102004\_083353\_5603 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	48.6	34	6	5256545-42 Patent No. 5256545
2	34	48.6	40	2	US-08-425-684-127 Sequence 127, App
3	34	48.6	40	2	US-08-675-502-127 Sequence 127, App
4	34	48.6	40	4	US-09-245-802-127 Sequence 127, App
5	34	48.6	41	1	US-08-168-917-16 Sequence 16, Appl
6	34	48.6	41	2	US-08-460-490-16 Sequence 16, Appl
7	34	48.6	41	2	US-08-460-490-16 Sequence 16, Appl
8	34	48.6	41	5	PCT-US92-00730-16 Sequence 16, Appl
9	34	48.6	41	5	PCT-US92-10430-11 Sequence 11, Appl
10	34	48.6	51	2	US-08-350-260A-287 Sequence 287, App
11	34	48.6	51	4	US-09-104-337A-287 Sequence 287, App
12	33	47.1	36	2	US-08-816-155B-38 Sequence 38, Appl

13	33	47.1	36	3	US-08-815-809-23 Sequence 23, Appl
14	33	47.1	36	3	US-09-079-587-38 Sequence 38, Appl
15	33	47.1	41	1	US-08-168-917-18 Sequence 18, Appl
16	33	47.1	41	2	US-08-460-510-18 Sequence 18, Appl
17	33	47.1	41	2	US-08-460-490-18 Sequence 18, Appl
18	33	47.1	41	5	PCT-US92-00730-18 Sequence 18, Appl
19	33	47.1	41	5	PCT-US92-10430-13 Sequence 13, Appl
20	32	45.7	33	4	US-09-566-420-2 Sequence 2, Appl
21	32	45.7	33	4	US-10-201-764-2 Sequence 2, Appl
22	32	45.7	33	4	US-08-422-978-2745 Sequence 2745, Ap
23	32	45.7	54	1	US-08-373-124A-2192 Sequence 2192, Ap
24	32	45.7	54	1	US-08-435-628-2192 Sequence 52, Appl
25	31	44.3	43	3	US-08-832-985-52 Sequence 52, Appl
26	31	44.3	43	4	US-09-410-903-33 Sequence 33, Appl
27	31	44.3	43	4	US-08-835-159-52 Sequence 31, Appl
28	31	44.3	47	1	US-08-093-884-31 Sequence 151, App
29	30	42.9	39	4	US-08-548-797B-151 Sequence 151, App
30	30	42.9	39	4	US-08-548-797B-152 Sequence 152, App
31	30	42.9	45	2	US-08-494-151-2 Sequence 2, Appl
32	30	42.9	47	4	US-09-422-978-522 Sequence 522, App
33	30	42.9	47	4	US-09-422-978-2073 Sequence 2073, Ap
34	30	42.9	50	2	US-08-709-368-2 Sequence 2, Appl
35	30	42.9	52	4	US-08-956-171E-2252 Sequence 2252, Ap
36	30	42.9	52	4	US-08-781-986A-2252 Sequence 2252, Ap
37	30	42.9	54	1	US-08-366-953A-23 Sequence 23, Appl
38	30	42.9	54	1	US-08-311-486C-1099 Sequence 29728, A
39	30	42.9	56	4	US-09-270-767-29728 Sequence 9, Appl
40	29.5	42.1	44	3	US-08-865-960-9 Sequence 70, Appl
41	29.5	42.1	55	2	US-08-850-049-70 Sequence 71, Appl
42	29.5	42.1	55	2	US-08-850-049-74 Sequence 74, Appl
43	29.5	42.1	55	2	US-08-050-478-70 Sequence 70, Appl
44	29.5	42.1	55	2	US-08-050-478-70 Sequence 71, Appl
45	29.5	42.1	55	2	US-08-050-478-71 Sequence 71, Appl

ALIGNMENTS

RESULT 1  
5256545-42  
; Patent No. 5256545  
; APPLICANT: BROWN, MICHAEL S.; GOLDSTEIN, JOSEPH L.; RUSSELL,  
; DAVID W.; SUDHOF, THOMAS C.  
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/425,852  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 33,330  
; FILING DATE: 30-MAR-1987  
; APPLICATION NUMBER: 33,081  
; FILING DATE: 30-MAR-1987  
; SEQ ID NO:42:  
; LENGTH: 34  
5256545-42

Alignment Scores: 61.2 Length: 34  
Pred. No.: 34.00 Matches: 7  
Score: 70.00% Conservatives: 0  
Percent Similarity: 70.00% Mismatches: 3  
Best Local Similarity: 48.57% Indels: 0  
Query Match: 6 Gaps: 0  
DB:

US-09-980-881A-9 (1-14) x 5256545-42 (1-34)

Qy 2 AsnProValGluLysLeuLeuProLeu 11  
|||  
Db 4 ATACCCCACTGCACAACTCTCCCTG 33  
|||||

RESULT 2  
US-08-425-684-127  
; Sequence 127, Application US/08425684

```
; Patent No. 5834252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN ESO., TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528J-015400US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-425-684-127

Alignment Scores:
Pred. No.: 75.3 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-425-684-127 (1-40)
Qy 3 ProProValGluLysLeuProLeuSer 12
Db 3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 3
US-08-675-502-127
; Sequence 127, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; Patent No. 5834252
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-675-502-127

Alignment Scores:
Pred. No.: 75.3 Length: 40
Score: 34.00 Matches: 5
Percent Similarity: 90.00% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 1
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-675-502-127 (1-40)
Qy 3 ProProValGluLysLeuProLeuSer 12
Db 3 CCGCCTTTGAGTGAGCTGATACCGCTCGCC 32

RESULT 4
US-09-245-802-127
; Sequence 127, Application US/09245802
; Patent No. 6489146
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

NAME: MURPHY, ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 16528J-015410US  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular

US-09-245-802-127

Alignment Scores:

Pred. No.: 75.3 Length: 40

Score: 34.00 Matches: 5

Percent Similarity: 90.00% Conservative: 4

Best Local Similarity: 50.00% Mismatches: 1

Query Match: 48.57% Indels: 0

DB: 4 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-245-802-127 (1-40)

Qy 3 ProProValGluLysLeuProLeuSer 12

Db 3 CCGCTTTCAGTACGCTGATACGCTCGCC 32

RESULT 5

US-08-168-917-16/c

Sequence 16, Application US/08168917

Patent No. 5686572

GENERAL INFORMATION:

APPLICANT: Wolf, David

APPLICANT: Tomlinson, James E.

APPLICANT: Fretto, Larry J.

APPLICANT: Giese, Neill A.

APPLICANT: Escobedo, Jaime A.

APPLICANT: Williams, Lewis T.

TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND

STREET: Steuart Street Tower, 20th Floor \ One Market

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/168,917

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/650,793

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: 12418-14

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
STRAIN: lambda gt10

US-08-168-917-16

Alignment Scores:

Pred. No.: 77.7 Length: 41

Score: 34.00 Matches: 6

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 75.00% Mismatches: 0

Query Match: 48.57% Indels: 0

DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-16 (1-41)

Qy 1 SerAsnProValGluLysLeu 8

Db 37 TCGATCCGCCAGTTAAGGAATT 14

RESULT 6

US-08-460-510-16/c

Sequence 16, Application US/08460510

Patent No. 5872218

GENERAL INFORMATION:

APPLICANT: Wolf, David

APPLICANT: Tomlinson, James E.

APPLICANT: Fretto, Larry J.

APPLICANT: Giese, Neill A.

APPLICANT: Escobedo, Jaime A.

APPLICANT: Williams, Lewis T.

TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW

STREET: One Market Plaza, Steuart Street Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,510

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 012418-001430

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

STRAIN: lambda gt10

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US-08-460-510-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-460-510-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAAC TT 14

RESULT 7
PCT-US92-00730-16/c
; Sequence 16, Application US/08460490
; Patent No. 5891852
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-460-510-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0

US-08-460-490-16/c
; Sequence 16, Application US/08460490
; Patent No. 5891852
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
US-08-460-490-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0

US-09-980-881A-9 (1-14) x US-08-460-490-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAAC TT 14

RESULT 8
PCT-US92-00730-16/c
; Sequence 16, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00730
; FILING DATE: 19920128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gt10
PCT-US92-00730-16
Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 5 Gaps: 0

US-09-980-881A-9 (1-14) x PCT-US92-00730-16 (1-41)
Qy 1 SerAsnProValGluLysLeu 8
Db 37 TCGAATCCGCCAGTTAAGGAAC TT 14
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RESULT 9
PCT-US92-10430-11
; Sequence 11, Application PC/TUS9210430
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: Methods for Production of Purified
; TITLE OF INVENTION: Soluble Type B and Type A Human Platelet-D
; TITLE OF INVENTION: Factor Receptor Fragments
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10430
; FILING DATE: 19921201
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,794
; FILING DATE: 02-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12418-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US92-10430-11

Alignment Scores:
Pred. No.: 77.7 Length: 41
Score: 34.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 48.57% Indels: 0
DB: 5 Gaps: 0

US-09-980-881A-9 (1-14) x PCT-US92-10430-11 (1-41)

Oy 1 SerAsnProProValGluLysLeu 8
Db 5 TCGAATCCGCCAGTTAAGGAAGCTT 28

RESULT 10
US-08-350-260A-287
; Sequence 287, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs

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; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-09-104-337A-287
Alignment Scores:
Pred. No.: 103 Length: 51
Score: 34.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 48.57% Indels: 0
DB: 4 Gaps: 0
US-09-980-881A-9 (1-14) x US-09-104-337A-287 (1-51)
Qy 3 ProProValGluLysLeuLeuProLeu 11
Db 11 CGCGGATACGAGTCTCCACTG 37
RESULT 12
US-08-816-155B-38
; Sequence 38, Application US/08816155B
; Patent No. 5990091
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; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; APPLICANT: GETTIG, RUSSELL R.
; APPLICANT: MARTINEZ, HECTOR
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: PINCUS, STEVEN E.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
; METHODS OF MAKING AND USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
; STREET: 745 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10151
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,155B
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-588-0800
; TELEFAX: 212-588-0500
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-816-155B-38
Alignment Scores:
Pred. No.: 101 Length: 36
Score: 33.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 47.14% Indels: 0
DB: 2 Gaps: 0
US-09-980-881A-9 (1-14) x US-08-816-155B-38 (1-36)
Qy 3 ProProValGluLysLeuLeuPro 10
Db 1 CCCCCTGCAGAAAAATTAGGCC 24
RESULT 13
US-08-815-809-23
; Sequence 23, Application US/08815809
; Patent No. 6004777
; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, James
; APPLICANT: GOEBEL, Scott J.
; APPLICANT: COX, William I.
; APPLICANT: GETTIG, Russell R.
; APPLICANT: PINCUS, Steven E.
; APPLICANT: PAOLETTI, Enzo
; APPLICANT: JACOBS, Bertram L.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
; MAKING AND USES THEREOF
; FILE REFERENCE: 454310-3010
; CURRENT APPLICATION NUMBER: US/08/815,809
; CURRENT FILING DATE: 1997-03-12
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NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 36  
TYPE: DNA  
ORGANISM: Vaccinia virus  
US-08-815-809-23

Alignment Scores:  
Pred. No.: 101 Length: 36  
Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-815-809-23 (1-36)

Qy 3 ProProValGluLysLeuLeuPro 10  
Db 1 CCCCTGCAGAAAAATTAGGCC 24

RESULT 14  
US-09-587-38  
Sequence 38, Application US/09079587  
Patent No. 6130066  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/816,155  
FILING DATE: 12-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-587-38  
Alignment Scores:  
Pred. No.: 101 Length: 36

Score: 33.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 3 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-079-587-38 (1-36)

Qy 3 ProProValGluLysLeuLeuPro 10  
Db 1 CCCCTGCAGAAAAATTAGGCC 24

RESULT 15  
US-08-168-917-18/c  
Sequence 18, Application US/08168917  
Patent No. 5686572  
GENERAL INFORMATION:  
APPLICANT: Wolf, David  
APPLICANT: Tomlinson, James E.  
APPLICANT: Pretto, Larry J.  
APPLICANT: Giese, Neill A.  
APPLICANT: Escobedo, Jaime A.  
APPLICANT: Williams, Lewis T.  
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN  
PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND  
STREET: Steuart Street Tower, 20th Floor \ One Market  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,917  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/650,793  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: 12418-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
STRAIN: lambda gt10  
US-08-168-917-18  
Alignment Scores:  
Pred. No.: 119 Length: 41  
Score: 33.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 47.14% Indels: 0

DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x US-08-168-917-18 (1-41)

Qy 1 SerAsnProProValGluLysLeuLeu 9

Db 37 TCGAATCCGCCAGTTATGATGTTGCTT 11

Search completed: October 26, 2004, 22:59:49  
Job time : 86 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 22:59:55 ; Search time 349 Seconds  
(without alignments)  
205.544 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVKLLPLSLK 14

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 1965782

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.spool\_p/US0980881/runat\_26102004\_083355\_5681/app\_query.fasta\_1.199  
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-TRANS-human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -WDB=DOCALLIGN -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=57 -USER=US0980881@cgn\_1\_1\_723@runat\_26102004\_083355\_5681 -NCPU=6  
-ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DGV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
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16: /cgn2\_6/ptodata1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata1/pubpna/US10E\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
C 1	46	65.7	43	10	US-09-845-064-24
C 2	37	52.9	41	16	US-10-035-833A-5237
C 3	35	50.0	45	9	US-09-978-295A-17
C 4	35	50.0	45	9	US-09-978-637-17
C 5	35	50.0	45	9	US-09-978-192A-17
C 6	35	50.0	45	9	US-09-999-832A-17
C 7	35	50.0	45	10	US-09-978-189-17
C 8	35	50.0	45	10	US-09-978-608A-17
C 9	35	50.0	45	10	US-09-978-585A-17
C 10	35	50.0	45	10	US-09-978-191A-17
C 11	35	50.0	45	10	US-09-978-403A-17
C 12	35	50.0	45	10	US-09-978-564A-17
C 13	35	50.0	45	10	US-09-999-833A-17
C 14	35	50.0	45	10	US-09-981-915A-17
C 15	35	50.0	45	10	US-09-978-824-17
C 16	35	50.0	45	10	US-09-918-585A-17
C 17	35	50.0	45	10	US-09-999-834A-17
C 18	35	50.0	45	10	US-09-978-423A-17
C 19	35	50.0	45	10	US-09-978-193A-17
C 20	35	50.0	45	10	US-09-999-830A-17
C 21	35	50.0	45	10	US-09-978-757A-17
C 22	35	50.0	45	10	US-09-978-187B-17
C 23	35	50.0	45	10	US-09-978-643A-17
C 24	35	50.0	45	10	US-09-978-375A-17
C 25	35	50.0	45	10	US-09-978-298A-17
C 26	35	50.0	45	10	US-09-978-188A-17
C 27	35	50.0	45	10	US-09-978-681A-17
C 28	35	50.0	45	10	US-09-978-194A-17
C 29	35	50.0	45	10	US-09-999-829A-17
C 30	35	50.0	45	10	US-09-978-544A-17
C 31	35	50.0	45	10	US-09-978-665A-17
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C 34	35	50.0	45	11	US-09-999-831A-17
C 35	35	50.0	45	14	US-10-017-081A-17
C 36	35	50.0	45	14	US-10-167-749-17
C 37	35	50.0	45	14	US-10-013-921A-17
C 38	35	50.0	45	14	US-10-013-929A-17
C 39	35	50.0	45	14	US-10-016-177A-17
C 40	35	50.0	45	15	US-10-166-709A-17
C 41	35	50.0	45	15	US-10-143-031A-17
C 42	35	50.0	45	15	US-10-002-967A-17
C 43	35	50.0	45	15	US-10-017-083A-17
C 44	35	50.0	45	15	US-10-145-128A-17
C 45	35	50.0	45	15	US-10-145-128A-17

ALIGNMENTS

RESULT 1  
US-09-845-064-24/c  
; Sequence 24, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Oligo  
; OTHER INFORMATION: Desoxynucleotide containing StuI restriction site

US-09-845-064-24

## Alignment Scores:

Pred. No.:	4.15	Length:	43
Score:	46.00	Matches:	9
Percent Similarity:	90.91%	Conservative:	1
Best Local Similarity:	81.82%	Mismatches:	1
Query Match:	65.71%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-845-064-24 (1-43)

Qy 1 SerAnProValGluLysLeuProLeu 11

Db 38 TCGAACCTCCGCGTAAGGCTTCTTACCATT 6

## RESULT 2

US-10-035-833A-5237/c

; Sequence 5237, Application US/10035833A

; Publication No. US20040072156A1

; GENERAL INFORMATION:

; APPLICANT: Nakamura, Yuho

; APPLICANT: Sekine, Akihiro

; APPLICANT: Iida, Aritoshi

; APPLICANT: Saito, Osamu

; TITLE OF INVENTION: Detection of Genetic Polymorphisms

; FILE REFERENCE: FORS-06904

; CURRENT APPLICATION NUMBER: US/10/035,833A

; CURRENT FILING DATE: 2001-12-27

; NUMBER OF SEQ ID NOS: 7669

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5237

; LENGTH: 41

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-035-833A-5237

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Best Local Similarity:	77.78%	Mismatches:	2
Query Match:	52.86%	Indels:	0
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US-09-980-881A-9 (1-14) x US-10-035-833A-5237 (1-41)

Qy 3 ProProValGluLysLeuProLeu 11

Db 33 CCACCTGTGGAGMCTTCTTACCACCTG 7

## RESULT 3

US-09-978-295A-17/c

; Sequence 17, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
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Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-295A-17 (1-45)

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Db 32 AGCAATGCCCGGTTCAAGGCGCTGCTCCCC 3

RESULT 4  
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; Sequence 17, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunes, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PlC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores: 45  
Pred. No.: 382 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-697-17 (1-45)

QY 1 SetAsnProValGluLysLeuLeuPro 10  
Db 32 AGCAATGCCCGCTTCAAGCCGTCCTCCC 3

RESULT 5

US-09-978-192A-17/c

Sequence 17, Application US/09978192A

Patent No. US2002017553A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Saton, Dan  
;; APPLICANT: Ferrara, Napoleon  
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;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.

;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C9  
;; CURRENT APPLICATION NUMBER: US/09/978,192A  
;; CURRENT FILING DATE: 2001-10-15  
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Alignment Scores:  
Pred. No.: 382 Length: 45  
Score: 35.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-192A-17 (1-45)  
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; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Nepier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.



APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Micky  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
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Pred. No.:      382      Length:      45
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Best Local Similarity: 70.00% Mismatches: 2
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US-09-980-881A-9 (1-14) x US-09-999-832A-17 (1-45)

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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Query Match: 50.00%  
DB: 10

Length: 45  
Matches: 7  
Conservative: 1  
Mismatches: 2  
Indels: 0  
Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-189-17 (1-45)  
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; Sequence 17, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-608A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-608A-17 (1-45)

QY 1 SerAnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 9
US-09-978-585A-17/c
; Sequence 17, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 17
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic oligonucleotide probe
US-09-978-585A-17

Alignment Scores:
Pred. No.: 382 Length: 45
Score: 35.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-585A-17 (1-45)

QY 1 SerAnProValGluLysLeuLeuPro 10
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

RESULT 10
US-09-978-191A-17/c
; Sequence 17, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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Alignment Scores: 382 Length: 45  
 Pred. No.: 35.00 Matches: 7  
 Score: 80.00% Conservative: 1  
 Percent Similarity: 80.00% Mismatches: 2  
 Best Local Similarity: 70.00% Indels: 0  
 Query Match: 50.00% Gaps: 0  
 DB: 10

US-09-980-881A-9 (1-14) x US-09-978-191A-17 (1-45)

Qy 1 SerAenProValGluLysLeuPro 10  
 Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCCC 3

# RESULT 11

US-09-978-403A-17/c

; Sequence 17, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

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; PRIOR FILING DATE: 1998-03-13  
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 ; PRIOR APPLICATION NUMBER: 60/078910  
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 ; PRIOR APPLICATION NUMBER: 60/078939  
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 ; PRIOR APPLICATION NUMBER: 60/079294  
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;; PRIOR APPLICATION NUMBER: 60/082700  
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;; PRIOR APPLICATION NUMBER: 60/082797  
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;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 382 Length: 45  
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Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0  
  
US-09-980-881A-9 (1-14) x US-09-978-403A-17 (1-45)  
  
Qy 1 SerAnProValGlulysLeuLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCC 3  
  
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US-09-978-564A-17/c  
; Sequence 17, Application US/09978564A  
; Publication No: US20030050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC25  
; CURRENT APPLICATION NUMBER: US/09/978,564A  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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8	PRIOR APPLICATION NUMBER: 60/079294	
9	PRIOR FILING DATE: 1998-03-25	
10	PRIOR APPLICATION NUMBER: 60/079656	
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12	PRIOR APPLICATION NUMBER: 60/079664	
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16	PRIOR APPLICATION NUMBER: 60/079663	
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23	PRIOR FILING DATE: 1998-03-30	
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33	PRIOR FILING DATE: 1998-03-31	
34	PRIOR APPLICATION NUMBER: 60/080327	
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50	PRIOR APPLICATION NUMBER: 60/081203	
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65	PRIOR FILING DATE: 1998-04-22	
66	PRIOR APPLICATION NUMBER: 60/082804	
67	PRIOR FILING DATE: 1998-04-22	
68	PRIOR APPLICATION NUMBER: 60/082700	
69	PRIOR FILING DATE: 1998-04-22	

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2	60/0821796	PRIOR FILING DATE: 1998-04-22	2	60/085700	PRIOR FILING DATE: 1998-05-15
3	60/082796	PRIOR APPLICATION NUMBER: 60/082796	3	60/085704	PRIOR APPLICATION NUMBER: 60/085704
4	60/082796	PRIOR FILING DATE: 1998-04-23	4	60/085733	PRIOR FILING DATE: 1998-05-15
5	60/083336	PRIOR APPLICATION NUMBER: 60/083336	5	60/085757	PRIOR APPLICATION NUMBER: 60/085757
6	60/083336	PRIOR FILING DATE: 1998-04-27	6	60/085869	PRIOR FILING DATE: 1998-05-15
7	60/083322	PRIOR APPLICATION NUMBER: 60/083322	7	60/085879	PRIOR APPLICATION NUMBER: 60/085879
8	60/083322	PRIOR FILING DATE: 1998-04-28	8	60/085892	PRIOR FILING DATE: 1998-05-15
9	60/083392	PRIOR APPLICATION NUMBER: 60/083392	9	60/085980	PRIOR APPLICATION NUMBER: 60/085980
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22	60/083559	PRIOR FILING DATE: 1998-04-29	22	60/085980	PRIOR FILING DATE: 1998-05-15
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26	60/083742	PRIOR FILING DATE: 1998-04-30	26	60/085980	PRIOR FILING DATE: 1998-05-15
27	60/084366	PRIOR APPLICATION NUMBER: 60/084366	27	60/085980	PRIOR FILING DATE: 1998-05-15
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Alignment Scores:

Pred. No.:

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**Length:**

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Length:  
Matches:

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Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-564A-17 (1-45)

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RESULT 13

US-09-999-833A-17/c

; Sequence 17, Application US/09999833A

; Publication No. US20030054405A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kiljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P26301C65

; CURRENT APPLICATION NUMBER: US/09/999,833A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

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; PRIOR APPLICATION NUMBER: 60/078886

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; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Length: 45  
Matches: 7  
Conservative: 1  
Mismatches: 2

Query Match: 50.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-980-881A-9 (1-14) x US-09-999-833A-17 (1-45)  
Qy 1 SerÅsenProValGluLysLeuLeuPro 10  
Db 32 AGCAATCCCGGTTCAAGGCGCTGCTCCCC 3  
RESULT 14  
US-09-981-915A-17/c  
; Sequence 17, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Sheiton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC12  
; CURRENT APPLICATION NUMBER: US/09/981.915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
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; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
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; PRIOR FILING DATE: 1998-03-13  
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; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
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; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR APPLICATION NUMBER: 60/082804  
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; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23

;  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
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; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	382	Length:	45
Score:	35.00	Matches:	7
Percent Similarity:	80.00%	Conservative:	1
Best Local Similarity:	70.00%	Mismatches:	2
Query Match:	50.00%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-9 (1-14) x US-09-981-915A-17 (1-45)

Qy 1 SerAsnProValGluLysLeuLeuPro 10  
||||| |||||::: |||||  
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCC 3

## RESULT 15

US-09-978-824-17/c

; Sequence 17, Application US/09978824

; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC14

; CURRENT APPLICATION NUMBER: US/09/978,824

; CURRENT FILING DATE: 2001-10-17

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/082797

; PRIOR FILING DATE: 1998-04-22

; PRIOR APPLICATION NUMBER: 60/082796

; PRIOR FILING DATE: 1998-04-23

; PRIOR APPLICATION NUMBER: 60/083336

; PRIOR FILING DATE: 1998-04-27

Thu Oct 28 07:16:19 2004

Qy 1 SerAsnProProValGluLysLeuPro 10  
Db 32 AGCAATGCCCGGTTCAAGGCTGCTCCC 3

Search completed: October 27, 2004, 01:00:47  
Job time : 353 secs

;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 382  
Score: 35.00  
Percent Similarity: 80.00%  
Best Local Similarity: 70.00%  
Query Match: 50.00%  
DB: 10

Length: 45  
Matches: 7  
Conservative: 1  
Mismatch: 2  
Indels: 0  
Gaps: 0

US-09-980-881A-9 (1-14) x US-09-978-824-17 (1-45)



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 00:51:05 ; Search time 39 Seconds  
(without alignments)  
34,539 Million cell updates/sec

Title: US-09-980-881A-9

Perfect score: 70

Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	41.4	13	2 B35245	histone H1.c - mou
2	28	40.0	19	2 S59485	hydroxyproline-rich
3	26	37.1	13	2 A35245	histone H1a - mous
4	26	37.1	14	2 C33098	223K exoantigen -
5	26	37.1	14	2 D61308	hemocyanin chain 5
6	25	35.7	14	2 S65392	cytochrome-c oxida
7	24.5	35.0	18	2 I52614	u-plasminogen acti
8	24	34.3	12	2 PA0098	ribosomal protein
9	23	32.9	10	2 S65715	aryl hydrocarbon (
10	23	32.9	18	2 S09026	carboxylesterase (
11	22	31.4	13	2 PT0331	Ig heavy chain CRD
12	22	31.4	15	2 S27248	pseudogargin - whe
13	22	31.4	15	2 PD0444	coupling factor 6
14	21	30.0	11	1 XASNBA	bradykinin-potent
15	21	30.0	11	2 I33098	173K exoantigen -
16	21	30.0	11	2 F33098	214K exoantigen (v
17	21	30.0	13	2 B19434	probable sex-speci
18	21	30.0	14	2 PA0111	protein QA100054 -
19	21	30.0	18	2 S56715	hydroxymethylgluta
20	20	28.6	8	2 S16324	hypothetical prote
21	20	28.6	9	2 S66419	tetrameric protein
22	20	28.6	10	2 S18396	probable glucose-6
23	20	28.6	10	2 C35389	urease (EC 3.5.1.5
24	20	28.6	10	2 B61218	alpha-gliadin 6Ha
25	20	28.6	13	2 A40207	cell surface glyco
26	20	28.6	14	4 I52618	hemoglobin beta ch
27	20	28.6	15	2 S05700	insulin-like growt
28	20	28.6	15	2 S20410	protein kinase (EC
29	20	28.6	15	2 G24417	interphotoreceptor

protein Pfl - gold  
insulin-like growt  
hypothetical COI/  
beta-Gliadin 13 -  
H+-transporting tw  
24K protein - List  
RNA polymerase bet  
N4-(beta-N-acetyl)  
MHC class I histoc  
crabrolin - Europe  
hemocyanin chain 2  
phosphoprotein, 80  
unidentified 22K p  
gene c-fms protein  
protein p12E - Pri  
blaz protein - Sta

ALIGNMENTS

RESULT 1

B35245

histone H1.c - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997

C:Accession: B35245

R:Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differ-

A:Reference number: A35245; MUID:90202935; PMID:1690730

A:Accession: B35245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <AVI>

C:Superfamily: histone H1

C:Keywords: chromosomal protein; nucleosome

Query Match 41.4%; Score 29; DB 2; Length 13;

Best Local Similarity 55.6%; Pred. No. 75;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKLL 9

Db 3 SGPPVSELI 11

RESULT 2

S59485

hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C>Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C:Accession: S59485; S59484; S59483

R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to differ-

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59485

A:Molecule type: protein

A:Residues: 1-19 <WOJ>

A:Cross-references: UNIPROT:Q7M1M8

A>Note: hydroxyproline-rich cell wall glycoprotein, 42K

A:Accession: S59484

A:Molecule type: protein

A:Residues: 1-15 <WOW>

A>Note: hydroxyproline-rich cell wall glycoprotein, 84K

A:Accession: S59483

A:Molecule type: protein

A:Residues: 1-14 <WOF>

A>Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component

C:Superfamily: proline-rich protein 3

C:Keywords: glycoprotein; hydroxyproline

F;6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 40.0%; Score 28; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPVEK 7  
 |||||  
 Db 5 PPVEK 9  
 |||||

RESULT 3  
 A35245  
 histone H1a - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
 C:Accession: A35245  
 R:Ajiro, K.; Shibata, K.; Nishikawa, Y.  
 J. Biol. Chem. 265, 6494-6500, 1990  
 A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentially phosphorylated serines  
 A:Reference number: A35245; PMID:1690730  
 A:Accession: A35245  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 <AJL>  
 C:Superfamily: histone H1  
 C:Keywords: chromosomal protein; nucleosome

Query Match 37.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNPPVEKLL 9  
 : |||||  
 Db 3 TGPPVSELI 11  
 : |||||

RESULT 4  
 C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: C33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: C33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <NIC>

Query Match 37.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPVEKL 8  
 |||||  
 Db 3 PPQEKL 8  
 |||||

RESULT 5  
 D61308  
 hemocyanin chain 5A - Sahara scorpion (fragment)  
 C:Species: Androctonus australis (Sahara scorpion)  
 C>Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004  
 C:Accession: D61308  
 R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
 FEBS Lett. 106, 289-291, 1979  
 A:Title: Structural characterization of seven different subunits in Androctonus australis  
 A:Reference number: A61308; PMID:80047238; PMID:499512  
 A:Accession: D61308  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <JOL>

A:Cross-references: UNIPROT:Q7M486

Query Match 37.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EKLLPL 11  
 |:||||  
 Db 7 ERLPL 12  
 |:||||

RESULT 6

S65392

cytochrome-c oxidase (EC 1.9.3.1) chain VIII-L - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 07-May-1999  
 C:Accession: S65392; S65393; S65391  
 R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
 Eur. J. Biochem. 230, 235-241, 1995  
 A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
 A:Reference number: S65372; PMID:95324529; PMID:7601105  
 A:Accession: S65392  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <SCH>  
 A:Accession: S65393  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <SC2>  
 A:Accession: S65391  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <SC3>  
 C:Keywords: oxidoreductase

Query Match 35.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNPPVEKL 8  
 |||||  
 Db 3 SKPPREQL 10  
 |||||

RESULT 7

I52614  
 u-plasminogen activator receptor precursor - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C:Accession: I52614  
 R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.  
 Blood 86, 624-635, 1995  
 A:Title: A conserved TATA-less proximal promoter drives basal transcription from the uro  
 A:Reference number: I52614; PMID:95329719; PMID:7605992  
 A:Accession: I52614  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-18 <RES>  
 A:Cross-references: UNIPROT:Q03405; GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g426198

C:Genetics:  
 C:Gene: uPAR  
 C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 35.0%; Score 24.5; DB 2; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 6.6e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 2 NPPVEKLPLSL 13  
 :|| |||||  
 Db 3 HPP---LLPULL 11  
 :|| |||||

RESULT 8



PA0098  
ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: PA0098  
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A:Reference number: PA0051  
A:Accession: PA0098  
A:Molecule type: protein  
A:Residues: 1-12 <CHO>  
A:Cross-references: UNIPROT:Q7M4X9

Query Match 34.3%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPVEKLPL 11  
| : ||| |  
Db 3 SPPVPKTFGL 12

RESULT 9  
S05715  
aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450 K(Ah) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 29-Oct-1999  
C:Accession: S05715  
R:Ohgaya, N.; Yokota, H.; Takahashi, M.; Komoro, S.; Yuasa, A.  
Biochim. Biophys. Acta 1209, 122-130, 1996  
A:Title: Purification and properties of a new beta-naphthoflavone inducible cytochrome P450  
A:Reference number: S05715; MUID:96195850; PMID:8605221  
A:Accession: S05715  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <OHG>  
C:Keywords: monooxygenase; oxidoreductase

Query Match 32.9%; Score 23; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PVEKLPL 10  
| : ||| |  
Db 4 PVXLLPL 10

RESULT 10  
S09026  
carboxylesterase (EC 3.1.1.1) MK1, microsomal - crab-eating macaque (fragment)  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S09026  
R:Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of Macaca fascicularis  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09026  
A:Molecule type: protein  
A:Residues: 1-18 <HOS>  
A:Cross-references: UNIPROT:Q7M2Q1  
C:Keywords: carboxylic ester hydrolase

Query Match 32.9%; Score 23; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPPV 5  
| : ||| |  
Db 3 SSPPV 7

## RESULT 11

PT0331  
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0331  
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J-segment in the generation of the human Ig heavy chain CRD3 region  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0331  
A:Molecule type: DNA  
A:Residues: 1-13 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPPVE 6  
| : ||| |  
Db 8 NNPPFQ 13

## RESULT 12

S27248  
pseudogerm - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 29-Aug-1997  
C:Accession: S27248  
R:Lane, B.G.; Cuming, A.C.; Fregeau, J.; Carpita, N.C.; Harkman, W.J.; Bernier, F.; Drat  
Eur. J. Biochem. 209, 961-969, 1992  
A:Title: Germ in isoforms are discrete temporal markers of wheat development. Pseudogerm  
ated embryos, it is incorporated into cell walls.  
A:Reference number: S27247; MUID:93049354; PMID:1425703  
A:Accession: S27248  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <LAN>

Query Match 31.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NPPVEKLPL 10  
| : ||| |  
Db 7 NNPPTPXXP 15

## RESULT 13

PD0444  
coupling factor 6 mitochondrial - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999  
C:Accession: PD0444  
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, August 1998  
A:Description: Proteome analysis of mouse brain.  
A:Reference number: PD0441  
A:Contents: Striatum  
A:Accession: PD0444  
A:Molecule type: protein  
A:Residues: 1-15 <KAW>  
C:Keywords: mitochondrion

Query Match 31.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVEKL 8  
| : ||| |  
Db 6 PVQKL 10

## RESULT 14

XASNBA  
bradykinin-potentiating peptide B - mamushi  
C:Species: Agkistrodon blomhoffi (mamushi)  
C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004  
C:Accession: A01254  
R:Kato, H.; Suzuki, T.  
Proc. Jpn. Acad. 46, 176-181, 1970  
A:Reference number: A01254  
A:Accession: A01254  
A:Molecule type: protein  
A:Residues: 1-11 <NR>  
A:Cross-references: UNIPROT:P01021  
A>Note: the sequence of the natural peptide was confirmed by the synthesis and analysis  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; vena  
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 21; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPVEKLLP 10  
|||  
DB 4 PPRPKIPP 11

## RESULT 15

I33098  
17k exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: I33098  
R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: I33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <NIC>

Query Match 30.0%; Score 21; DB 2; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPVEKLLPL 11  
|||  
DB 3 PPELPLFFI 11

Search completed: October 27, 2004, 01:06:06  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 26, 2004, 22:25:16 ; Search time 2863 Seconds  
(without alignments)  
178.189 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEXKLPLSLK 14

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 214274

Minimum DB seq length: 0  
Maximum DB seq length: 57

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DBV=slp  
-Q/cgn2\_1/USPTO.spool\_p/US09980881/runat\_26102004\_083353\_5586/app\_query.fasta\_1.199  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=57  
-USER=US09980881@cgn\_1\_1\_5180@runat\_26102004\_083353\_5586 -NCPU=6 -ICPU=3  
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Database : EST:  
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2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	40	57.1	55	9 CR221258	Forward s
C 2	38	54.3	50	1 AU107009	AU107009 AU107009
C 3	35	50.0	56	8 AZ808573	AZ808573 2M0072K08
C 4	33	47.1	43	1 AI655018	AI655018 wb66b02.x
C 5	33	47.1	43	9 TA279C01P	TA279C01P
C 6	33	47.1	44	9 CL675662	CL675662 PRI0115C
C 7	33	47.1	49	1 AA482011	AA482011 zu98c07.s
C 8	33	47.1	52	1 AA897173	AA897173 am09d08.s
C 9	33	47.1	53	9 CR026397	CR026397 Forward s

10	33	47.1	56	6 CF314148	CF314148 HD--02-J0
11	33	47.1	56	7 CF886287	CF886287 tr1c086xc
12	32.5	46.4	50	7 CN869022	CN869022 001202AAO
C 13	32	45.7	31	1 A1760292	A1760292 wg59f03.x
C 14	32	45.7	38	8 A2964138	A2964138 2M0233N11
C 15	32	45.7	43	9 CL654491	CL654491 PRI0120C
C 16	32	45.7	45	9 AU590579	AU590579 Arabidops
C 17	32	45.7	48	8 BH790348	BH790348 SALK_0568
C 18	32	45.7	49	1 AA865390	AA865390 oh49f11.s
C 19	32	45.7	50	1 AU107993	AU107993 AU107993
C 20	32	45.7	51	1 AV528824	AV528824 AV528824
C 21	32	45.7	53	1 AL965914	AL965914 AL965914
C 22	31	44.3	41	9 BX943466	BX943466 Arabidops
C 23	31	44.3	50	6 CD029909	CD029909 mgmko16xm
C 24	31	44.3	50	8 A2805497	A2805497 2M0066K19
C 25	31	44.3	50	9 CR148320	CR148320 Forward s
C 26	31	44.3	53	9 BX891907	BX891907 Arabidops
C 27	31	44.3	54	7 CN756377	CN756377 ID0AAAL18C
C 28	31	44.3	55	1 AU789274	AU789274 AU789274
C 29	31	44.3	57	7 CR429117	CR429117 CR429117
C 30	30	42.9	34	8 A2832181	A2832181 2M0112K19
C 31	30	42.9	43	4 BI460424	BI460424 603200910
C 32	30	42.9	45	9 BX945468	BX945468 Arabidops
C 33	30	42.9	45	9 CR356909	CR356909 Arabidops
C 34	30	42.9	48	8 BH627451	BH627451 100707180
C 35	30	42.9	48	8 BH904904	BH904904 SALK_1053
C 36	30	42.9	50	1 A1174165	A1174165 vz84f07.r
C 37	30	42.9	50	1 AU107434	AU107434 AU107434
C 38	30	42.9	50	8 A2767297	A2767297 1M0566G21
C 39	30	42.9	51	8 BH218345	BH218345 1006078E0
C 40	30	42.9	52	7 CN750625	CN750625 ApDT-XX-H
C 41	30	42.9	52	9 AG248432	AG248432 Lotus cor
C 42	30	42.9	53	6 CA840659	CA840659 MCT039H07
C 43	30	42.9	54	8 A2579138	A2579138 1M0363C03
C 44	30	42.9	55	1 AA937358	AA937358 oi08e10.s
C 45	30	42.9	55	9 CL293965	CL293965 02S0349-0

ALIGNMENTS

RESULT 1  
CR221258/c

LOCUS  
DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CR221258 55 bp DNA linear GSS 06-JUL-2004  
Forward strand read from insert in 5'HPRT insertion targeting and  
chromosome engineering clone MHPN238119, genomic survey sequence.

CR221258.1 GI:50000107  
GSS; Genome survey sequence; MICER.  
Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 55)  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

Direct Submission  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

Location/Qualifiers  
1..55  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPN238119"

Alignment Scores:  
Pred. No.: 681  
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Percent Similarity: 81.82%  
Best Local Similarity: 72.73%

Length: 55  
Matches: 8  
Conservative: 1  
Mismatch: 2

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US-09-980-881A-9 (1-14) x CR221258 (1-55)

Qy      3  ProProValGlulysLeuLeuProLeuSerLeu 13
Db      50  CCCCCCAGCAATCCCTACTCTCTCTCACTC 18

RESULT 2
LOCUS   AU107009 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
ACCESSION ZRV6C668, mRNA sequence.
VERSION   AU107009
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Tajira,H., Tsunoda,T., Mizushima-Sugano,J., See,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,F., Nakamura,F., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL  21270072
MEDLINE  11375929
PUBMED   11375929
COMMENT   Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             Location/Qualifiers
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                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Alignment Scores:
Pred. No.:      1.37e+03      Length:      50
Score:          38.00        Matches:      8
Percent Similarity: 90.00%    Conservative: 1
Best Local Similarity: 80.00% Mismatches:  1
Query Match:    54.23%        Indels:      0
Db:             1          Gaps:      0

US-09-980-881A-9 (1-14) x AU107009 (1-50)

Qy      3  ProProValGlulysLeuLeuProLeuSer 12
Db      15  CCGTGTGTGGAGAACTGCTGCGGTGTCA 44

RESULT 3
LOCUS   AZ808573
DEFINITION
ACCESSION AZ808573
VERSION   AZ808573.1 GI:12974037
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: K column: 08
Seq Primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 56.
Location/Qualifiers
     source           1..56
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0072K08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.:      5.33e+03      Length:      56
Score:          35.00        Matches:      7
Percent Similarity: 64.29%    Conservative: 2
Best Local Similarity: 50.00% Mismatches:  5
Query Match:    50.00%        Indels:      0
Db:             8          Gaps:      0

US-09-980-881A-9 (1-14) x AZ808573 (1-56)

Qy      1  SerAsnProProValGlulysLeuLeuProLeuSerLeuLys 14
Db      15  TCAAAATCCCCCCCCACATATAAATCATCCCTCATCTCGCAA 56

RESULT 4
LOCUS   AI655018
DEFINITION
wb66b02.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2310603 3',
similar to TR:O35295 O35295 VASCULAR ACTIN SINGLE-STRANDED
DNA-BINDING FACTOR 2 P44 COMPONENT. ;, mRNA sequence.

```

**ACCESSION** AI655018  
**VERSION** AI655018.1 GI:4738997  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 43)  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..43  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2310603"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GC6"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 8,75e+03 Length: 43  
 Score: 33.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 60.00% Mismatches: 3  
 Query Match: 47.14% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-980-881A-9 (1-14) x AI655018 (1-43)  
 Qy 3 ProProValGlulysLeuLeuProLeuSer 12  
 Db 3 CCGCCCTGCGTGGCGTGGCTGCGCTGCTG 32  
 RESULT 5  
 TA279C01P 43 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 279c01, forward sequence, genomic survey sequence.  
 DEFINITION  
 ACCESSION AL487206 GI:11852258  
 VERSION AL487206.1  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

**REFERENCE** 1 (bases 1 to 43)  
**AUTHORS** Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
**COMMENT** Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In: Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).  
 Location/Qualifiers  
 1..43  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="279C01"

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 8,75e+03 Length: 43  
 Score: 33.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 47.14% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-980-881A-9 (1-14) x TA279C01P (1-43)  
 Qy 3 ProProValGlulysLeuLeuPro 10  
 Db 13 CCCCCCTTTTCAAACTCTCCCT 36  
 RESULT 6  
 CL675662 44 bp DNA linear GSS 09-JUL-2000  
 LOCUS PRI0115C\_B08.2 - PRI0115C.BR (44) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
 DEFINITION  
 ACCESSION CL675662 GI:50180358  
 VERSION CL675662.1  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
**REFERENCE** 1 (bases 1 to 44)  
**AUTHORS** Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
**TITLE** AppADB: an AcedB database for the nematode satellite organism Pristionchus pacificus  
**JOURNAL** Nucleic Acids Res. 32 (1), D421-D422 (2004)  
**COMMENT** Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

```

FEATURES
source
Location/Qualifiers
1. .44
/organism="Prionostichus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Alignment Scores:
Pred. No.: 9e+03 Length: 44
Score: 33.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 47.14% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CL675662 (1-44)

QY 1 SerAnProValGluLysLeuProLeuSer 12
|||||
8 TCCCCCCCCCCCTAAATAAAGTCTGCTCGATCA 3

Db

RESULT 7
AA482011
LOCUS
DEFINITION
AA482011 49 bp mRNA linear EST 14-AUG-1997
zu98c07.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:746028 3'
similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN);, mRNA
sequence.
ACCESSION
AA482011
VERSION
AA482011.1 GI:2209689
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
REFERENCE
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5945466"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI-CGAP GCBI"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

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(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGCGGCGCTCATTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Alignment Scores:
Pred. No.: 1.02e+04 Length: 49
Score: 33.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 47.14% Indels: 0
DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x AA482011 (1-49)

QY 1 SerAnProValGluLysLeuProLeuSerLeu 13
|||||
8 TCAATGATCCTTTTATTGAAATGTTTCTTTGGCTTA 46

Db

RESULT 8
AA897173/c
LOCUS
DEFINITION
AA897173 52 bp mRNA linear EST 07-APR-1998
am09d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1466319 3' similar to SW:ACY2_HUMAN P45381 ASPARTOACYLASE ;,
mRNA sequence.
ACCESSION
AA897173
VERSION
AA897173.1 GI:3033793
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 52)
REFERENCE
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
JOURNAL
Unpublished (1997)
COMMENT
Contact: Wilton RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .52
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1466319"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: p7T73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung N8HL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of

```

I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Donaldo.

## ORIGIN

## Alignment Scores:

Pred. No.: 1.1e+04 Length: 52  
Score: 33.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 47.14% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-9 (1-14) x AA897173 (1-52)

Qy 6 GluLyLeuLeuProLeuSerLeu 13

Db 24 GAGAAATTTCTTCCTTTATCCCTC 1

## RESULT 9

CR026397/c

LOCUS

DEFINITION Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPPI35d08, genomic survey sequence.

ACCESSION CR026397

VERSION CR026397.1 GI:49759452

KEYWORDS GSS; genome survey sequence; MICR.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 53)

AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,

Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,

Rogers,J., and Bradley,A.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICR

## FEATURES

source  
1..53  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone\_lib="MHPPI35d08"  
/clone\_lib="MHPPI"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.13e+04 Length: 53  
Score: 33.00 Matches: 5  
Percent Similarity: 80.00% Conservative: 3  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 47.14% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-9 (1-14) x CR026397 (1-53)

Qy 3 ProProValGluLyLeuLeuProLeuSer 12

Db 47 CCCCCCTTGACTCTCTTGTCCCATATCA 18

## RESULT 10

CF314148

LOCUS

DEFINITION HD-02-J02.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD-02-J02, mRNA sequence.

ACCESSION CF314148

VERSION CF314148.1 GI:33685909

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 56)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

## source

1..56

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="HD-02-J02"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr- Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

## ORIGIN

## Alignment Scores:

Pred. No.: 1.2e+04 Length: 56  
Score: 33.00 Matches: 5  
Percent Similarity: 60.00% Conservative: 1  
Best Local Similarity: 50.00% Mismatches: 4  
Query Match: 47.14% Indels: 0  
DB: 6 Gaps: 0

US-09-980-881A-9 (1-14) x CF314148 (1-56)

Qy 2 AnProProValGluLyLeuLeuProLeu 11

Db 22 AATCCCCCAATCCGATCTGCTTCTCTT 51

## RESULT 11

CF886287

LOCUS

DEFINITION

tric086xc09.g1 T-reesei mycelial culture, Version 6 October 2003

Hypocrea jecorina cDNA clone tric086xc09, mRNA sequence.

ACCESSION

CF886287

VERSION

CF886287.1

KEYWORDS

EST.

SOURCE

ORGANISM

Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE

AUTHORS

1 (bases 1 to 56)

Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,

Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,

Ward,M. and Dean,R.A.

Characterization of the protein processing and secretion pathways

in a comprehensive set of expressed sequence tags from Trichoderma

reesei

FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

JOURNAL

COMMENT

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

```

Email: ralph.dean@ncsu.edu
Seq primer: LR-R1 primer.
Location/Qualifiers
FEATURES
    source
        1..56
            /organism="Hypocrea jecorina"
            /mol_type="mRNA"
            /strain="QM6a"
            /db_xref="taxon:51453"
            /clone="trico86xc09"
            /dev_stage="mycelia"
            /clone_lib="T.reesei mycelial culture, Version 6 October 2003"
            /note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
ORIGIN
Alignment Scores:
Pred. No.: 1.2e+04 Length: 56
Score: 33.00 Matches: 5
Percent Similarity: 88.89% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 1
Query Match: 47.14% Indels: 0
DB: 7 Gaps: 0

US-09-980-881a-9 (1-14) x CF886287 (1-56)
Qy 2 AsnProProValGluLysLeuLeuPro 10
Db 9 AATCCGCTATATAAATAAGTGCT 35

RESULT 12
CN869022 50 bp mRNA linear EST 03-JUN-2004
LOCUS 001202AAOA004091HT (AAOA) Royal Gala phloem Malus x domestica cDNA
DEFINITION clone AAOA004091, mRNA sequence.
ACCESSION CN869022
VERSION CN869022.1 GI:48126603
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES
    source
        1..50
            /organism="Malus x domestica"
            /mol_type="mRNA"
            /db_xref="taxon:3750"
            /clone="AAOA004091"
            /tissue_type="Phloem, scrapings from inside of bark mature wood"
            /clone_lib="(AAOA) Royal Gala phloem"
            /note="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"
ORIGIN
Alignment Scores:
Pred. No.: 1.29e+04 Length: 50
Score: 32.50 Matches: 6
Percent Similarity: 91.67% Conservative: 5

Email: ralph.dean@ncsu.edu
Seq primer: LR-R1 primer.
Location/Qualifiers
FEATURES
    source
        1..56
            /organism="Hypocrea jecorina"
            /mol_type="mRNA"
            /strain="QM6a"
            /db_xref="taxon:51453"
            /clone="trico86xc09"
            /dev_stage="mycelia"
            /clone_lib="T.reesei mycelial culture, Version 6 October 2003"
            /note="Vector: pREP3Y, Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
ORIGIN
Alignment Scores:
Pred. No.: 1.2e+04 Length: 56
Score: 33.00 Matches: 5
Percent Similarity: 88.89% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 1
Query Match: 47.14% Indels: 0
DB: 7 Gaps: 0

US-09-980-881a-9 (1-14) x CF886287 (1-56)
Qy 2 AsnProProValGluLysLeuLeuPro 10
Db 9 AATCCGCTATATAAATAAGTGCT 35

RESULT 12
CN869022 50 bp mRNA linear EST 03-JUN-2004
LOCUS 001202AAOA004091HT (AAOA) Royal Gala phloem Malus x domestica cDNA
DEFINITION clone AAOA004091, mRNA sequence.
ACCESSION CN869022
VERSION CN869022.1 GI:48126603
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES
    source
        1..50
            /organism="Malus x domestica"
            /mol_type="mRNA"
            /db_xref="taxon:3750"
            /clone="AAOA004091"
            /tissue_type="Phloem, scrapings from inside of bark mature wood"
            /clone_lib="(AAOA) Royal Gala phloem"
            /note="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"
ORIGIN
Alignment Scores:
Pred. No.: 1.29e+04 Length: 50
Score: 32.50 Matches: 6
Percent Similarity: 91.67% Conservative: 5

Best Local Similarity: 50.00% Mismatches: 0
Query Match: 46.43% Indels: 1
DB: 7 Gaps: 1

US-09-980-881a-9 (1-14) x CN869022 (1-50)
Qy 2 AsnProProValGluLysLeuLeu---ProLeuSer 12
Db 14 TCTCCTCAATTGAGCAAAATTATTATATCCCTTTCA 49

RESULT 13
AT1760292/2
LOCUS AT1760292/2 31 bp mRNA linear EST 20-DEC-1999
DEFINITION WG59f03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens CDNA clone IMAGE:2369405 3' similar to SW:D3D2 HUMAN P42126 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR 1, mRNA sequence.
ACCESSION AT1760292
VERSION AT1760292.1 GI:5175959
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1200 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
    'source
        1..31
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2369405"
            /lab_host="DH10B"
            /clone_lib="Soares NSF_F8_9W_OT_PA_P_S1"
            /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HP8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 8.85e+03 Length: 31
Score: 32.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 45.71% Indels: 0
DB: 1 Gaps: 0

US-09-980-881a-9 (1-14) x AT1760292 (1-31)

```



```

Qy 3 ProProValGlulysLeuPro 10
    |||||:||||:|||||
Db 29 CCCCCTTAAGACAGCTTAAGCT 6

RESULT 14
AZ964138 38 bp DNA linear GSS 27-APR-2001
LOCUS 2M0233N11R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0233N11 R, genomic survey sequence.
ACCESSION AZ964138
VERSION AZ964138.1 GI:13835365
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: N column: 11
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES             Location/Qualifiers
     1..38
         /organism="Mus musculus"
         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0233N11"
         /sex="Female"
         /lab_host="E. coli strain XL10-Gold, T1-resistant, P-"
         /clone_lib="Mouse 10kb plasmid UUGC2M library"
         /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 1.13e+04 Length: 38
Score: 32.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0

```

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Query Match: 45.71% Indels: 0
DB: 8 Gaps: 0
US-09-980-881A-9 (1-14) x AZ964138 (1-38)

Qy 6 GlulysLeuProLeuSerLeu 13
    ::|||:|||||
Db 1 CAGAAATATTACCTCTCTCTC 24

RESULT 15
CL654491/c 43 bp DNA linear GSS 09-JUL-2004
LOCUS PR10120c_H04 - PR10120c.B21 (43) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL654491
VERSION CL654491.1 GI:50133440
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
AUTHORS Neodiplogasteridae; Pristionchus.
1 (bases 1 to 43)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL Contact: Sommer RJ
COMMENT Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES             Location/Qualifiers
     1..43
         /organism="Pristionchus pacificus"
         /mol_type="genomic DNA"
         /strain="California"
         /db_xref="taxon:54126"
         /clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
         /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Alignment Scores:
Pred. No.: 1.31e+04 Length: 43
Score: 32.00 Matches: 7
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 58.33% Mismatches: 4
Query Match: 45.71% Indels: 0
DB: 9 Gaps: 0
US-09-980-881A-9 (1-14) x CL654491 (1-43)

Qy 2 AsnProValGlulysLeuProLeuSerLeu 13
    ::|||
Db 39 TCCCTCTCTCTCTCTCTCTCTCTCTCTC 4

Search completed: October 26, 2004, 23:47:45
Job time : 2867 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2004, 23:47:55 ; Search time 134 Seconds  
(without alignments)  
60.114 Million cell updates/sec

Title: US-09-980-881A-9  
Perfect score: 70  
Sequence: 1 SNPPVEKLLPLSLK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 12441

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	40.0	14	2	Q16232 homo sapien
2	28	40.0	19	2	Q7M1M8 phaseolus v
3	28	40.0	19	2	Q9S8G9 psophocarpu
4	26.5	37.9	19	2	Q94106 brassica na
5	26	37.1	14	2	Q7M486 androctonus
6	25	35.7	10	1	Q7M486 canis fami
7	25	35.7	10	1	Q8CJEO rattus norv
8	25	35.7	11	2	Q8IVG8 homo sapien
9	25	35.7	11	2	Q47604 escherichia
10	25	35.7	11	2	Q47604 escherichia
11	25	35.7	15	2	Q714T7 prionitis l
12	25	35.7	15	2	Q714T7 prionitis l
13	24	34.3	12	2	Q7M4X9 fusarium sp
14	24	34.3	16	2	Q8KXP2 clostridium
15	24	34.3	16	2	Q9QY8 cricetus
16	24	34.3	16	2	Q6WV37 simian t-ly
17	24	34.3	16	2	Q6WV42 simian t-ly
18	24	34.3	16	2	Q6WV42 simian t-ly
19	24	34.3	16	2	Q6WV42 simian t-ly
20	24	34.3	16	2	Q6WV42 simian t-ly
21	24	34.3	18	1	PCG6_PACGO
22	24	34.3	18	2	Q8CJ44 rattus norv
23	24	34.3	19	1	PCG7_PACGO
24	23	32.9	15	2	Q8RKN0 escherichia
25	23	32.9	16	2	P79034 emericella
26	23	32.9	18	2	Q7M201 macaca fasc
27	23	32.9	18	2	Q41588 human immu
28	23	32.9	19	2	Q9BDX2 macaca mula
29	23	32.9	19	2	Q33755 streptococ
30	22	31.4	14	2	Q35917 rattus norv
31	22	31.4	15	1	UC17_MAIZE

Q61a1l drosophila  
Caa76424 drosophil  
Caa76430 drosophil  
Caa76436 drosophil  
Caa76442 drosophil  
Caa76448 drosophil  
Caa76454 drosophil  
Caa76460 drosophil  
Caa76466 drosophil  
Caa76476 drosophil  
Q8J696 human t-lym  
Q8J697 human t-lym  
Q8J698 human t-lym  
Q8J699 human t-lym

## ALIGNMENTS

### RESULT 1

Q16232 PRELIMINARY; PRT; 14 AA.  
AC Q16232  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE NF2 protein (Fragment).  
GN Name=NF2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94348501; PubMed=8069299;  
RA Arakawa H., Hayashi N., Nagase H., Ogawa M., Nakamura Y.;  
RT "Alternative splicing of the NF2 gene and its mutation analysis of  
RT breast and colorectal cancers.";  
RL Hum. Mol. Genet. 3:565-568(1994).  
DR EMBL, S73855; AAD14139.1; -;  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1513 MW; 82766855653CBB2A CRC64;

Query Match 40.0%; Score 28; DB 2; Length 14;  
Best Local Similarity 58.3%; Pred. No. 8.1e+02;  
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPVEKLLPLSLK 14  
| | | | |  
Db 3 PRAEDLSALSLSK 14

### RESULT 2

Q7M1M8 PRELIMINARY; PRT; 19 AA.  
AC Q7M1M8  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hydroxyproline-rich cell wall glycoprotein (42k and others) (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96011753; PubMed=7548825;  
RA Wojtaszek P., Trehowan J., Bolwell G.P.;  
RT "Specificity in the immobilisation of cell wall proteins in response  
RT to different elicitor molecules in suspension-cultured cells of French  
RT bean (Phaseolus vulgaris L.).";

RL Plant Mol. Biol. 28:1075-1087(1995).

DR PIR; SS9485; SS9485.

FT NON\_TER 1

FT NON\_TER 19

SQ SEQUENCE 19 AA; 2225 MW; 53AB9D0984A87E0A CRC64;

Query Match 40.0%; Score 28; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7

Db 5 PPVEK 9

RESULT 3

Q9S8G9

ID Q9S8G9 PRELIMINARY; PRT; 19 AA.

AC Q9S8G9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Proline-rich protein (Fragment).

OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

OC Psophocarpus.

OX NCBI\_TaxID=3891;

RN [1]

RP SEQUENCE.

RX MEDLINE=95277008; PubMed=7757337;

RA Esaka M., Hayakawa H.;

RT "Specific secretion of proline-rich proteins by salt-adapted winged

bean cells.";

RL Plant Cell Physiol. 36:441-446(1995).

SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 19;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPVEK 7

Db 5 PPVEK 9

RESULT 4

Q94L06

ID Q94L06 PRELIMINARY; PRT; 19 AA.

AC Q94L06;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Isopropyl malate synthase (Fragment).

GN Name=M024-1-BN-7;

OS Brassica napus (Rape).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Brassica.

OX NCBI\_TaxID=3708;

RN [1]

RP SEQUENCE FROM N.A.

RA Fourmann M., Froger N., Brunel D.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF258256; AAK49052.1; --

FT NON\_TER 1

FT NON\_TER 19

SQ SEQUENCE 19 AA; 1989 MW; A41FC1E46CFC0E6D CRC64;

Query Match

Best Local Similarity 46.2%; Score 26.5; DB 2; Length 19;

Matches 6; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2 NPPVEKLLPLSLK 14

Db 3 NAPLEKVV-MALK 14

RESULT 5

Q7M486

ID Q7M486 PRELIMINARY; PRT; 14 AA.

AC Q7M486;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hemocyanin chain 5A (Fragment).

OS Androctonus australis (Sahara scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthida; Buthoidea; Buthidae; Androctonus.

OX NCBI\_TaxID=6858;

RN [1]

RP SEQUENCE.

RA Jolles J., Jolles P., Lamy J., Lamy J.;

RT "Structural characterization of seven different subunits in

Androctonus australis haemocyanin.";

RL FEBS Lett. 106:289-291(1979).

DR PIR; D61308; D61308.

FT NON\_TER 1

FT NON\_TER 14

SQ SEQUENCE 14 AA; 1658 MW; 6FA4342770FEAF0B CRC64;

Query Match

Best Local Similarity 37.1%; Score 26; DB 2; Length 14;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EKLPL 11

Db 7 ERLPL 12

RESULT 6

CX82\_CANFA

ID CX82\_CANFA STANDARD; PRT; 10 AA.

AC P61905;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cytochrome c oxidase polypeptide VIII-liver (EC 1.9.3.1) (Cytochrome c

oxidase subunit 8-2) (Fragment).

GN Name=COX8A;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=96092035; PubMed=8529022;

RA Linder D., Freund R., Kadenbach B.;

RT "Species-specific expression of cytochrome c oxidase isozymes.";

Comp. Biochem. Physiol. 112B:461-469(1995).

CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide

chains of cytochrome c oxidase, the terminal oxidase in

mitochondrial electron transport.

CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) = 4 ferricytochrome

c + 2 H(2)O.

CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -!- TISSUE SPECIFICITY: Liver specific isoform.

CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.

KW Direct protein sequencing; Inner membrane; Mitochondrion;

Oxidoreductase.

FT NON\_TER 10

SQ SEQUENCE 10 AA; 1204 MW; 9304F6041776325 CRC64;

Query Match

35.7%; Score 25; DB 1; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKL 8  
Db 3 SKPPREQL 10

RESULT 7  
ID Q8CJEO PRELIMINARY; PRT; 10 AA.  
AC Q8CJEO;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Resibitin (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Nohira T., Hisatomi H.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB093559; BAC21195.1; -.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1079 MW; 34EA46D326DDC777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPVEKL 10  
Db 3 PPAQKAQP 10

RESULT 8  
ID Q8IVG8 PRELIMINARY; PRT; 11 AA.  
AC Q8IVG8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Low density lipoprotein receptor related protein 1 (lipoprotein receptor-related protein) (Fragment).  
GN Name=LRP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Glaeser C.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Schulz S.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RX MEDLINE=90089395; PubMed=2597675;  
RA Kuett H.C., Herz J., Stanley K.K.;  
RT "Structure of the low-density lipoprotein receptor-related protein (LRP) promoter.";  
RL Biochim. Biophys. Acta 1009:229-236 (1989).  
DR EMBL; Y18524; CAD57169.1; -.  
EMBL; X15424; CAA33464.1; -.

DR CO; GO:0004872; F:receptor activity; IEA.  
KW Lipoprotein; Receptor.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PPVEKL 10  
Db 4 PPLLLLP 11

RESULT 9  
ID Q47604 PRELIMINARY; PRT; 11 AA.  
AC Q47604;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN Name=REase;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-modification systems.";  
RL J. Bacteriol. 173:1367-1375 (1991).  
DR EMBL; M63621; AAA24560.1; -.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 2.1e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPPVEKL 9  
Db 2 SHPDINKLL 10

RESULT 10  
ID CAA33464 PRELIMINARY; PRT; 11 AA.  
AC CAA33464;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Lipoprotein receptor-related protein (Fragment).  
GN LRP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RA Kuett H.C., Herz J., Stanley K.K.;  
RT "Structure of the low-density lipoprotein receptor-related protein (LRP) promoter.";  
RL Biochim. Biophys. Acta 1009:229-236 (1989).  
DR EMBL; X15424; CAA33464.1; -.  
KW Receptor.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 2.1e+03; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVEKLLP 10  
||: |||  
Db 4 PELLLLP 11

## RESULT 11

ID Q714T7 PRELIMINARY; PRT; 15 AA.  
AC Q714T7; 05-JUL-2004 (TremBLrel. 27, Created)  
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
DE Tmrna proteolysis tag (Fragment).  
GN Name=ssrA;  
OS Prionitis lanceolata.  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;  
OC Prionitis.  
OX NCBI\_TaxID=31457;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14681369;  
RA Gueneau de Novoa P., Williams K.P.;  
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts.";  
RL Nucleic Acids Res. 32:D104-D108(2004).  
DR EMBL; AF550353; AAQ12669.1; --  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1659 MW; 44990BB95D14E2B2 CRC64;

Query Match 35.7%; Score 25; DB 2; Length 15;

Best Local Similarity 62.5%; Pred. No. 3e+03; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLLPLSLK 14  
::||| |  
Db 4 QILPLSRK 11

## RESULT 12

AAQ12669 PRELIMINARY; PRT; 15 AA.  
AC AAQ12669;  
DT 02-MAR-2004 (TremBLrel. 27, Created)  
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)  
DE Tmrna proteolysis tag (Fragment).  
GN SSRA.  
OS Prionitis lanceolata.  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;  
OC Prionitis.  
OX NCBI\_TaxID=31457;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14681369;  
RA Gueneau de Novoa P., Williams K.P.;  
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts.";  
RL Nucleic Acids Res. 32:D104-D108(2004).  
DR EMBL; AF550353; AAQ12669.1; --  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1659 MW; 44990BB95D14E2B2 CRC64;

Query Match

Best Local Similarity 62.5%; Score 25; DB 2; Length 15;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 KLLPLSLK 14

Db 4 QILPLSRK 11  
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## RESULT 13

Q7M4X9 PRELIMINARY; PRT; 12 AA.  
AC Q7M4X9; 01-MAR-2004 (TremBLrel. 26, Created)  
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Ribosomal protein S3 (Fragment).  
OS Fusarium sporotrichioides.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
OX NCBI\_TaxID=5514;  
RN [1]  
RP SEQUENCE.  
RA Chow L.P., Fukaya N., Sugiura Y., Ueno Y., Tabuchi K., Taugita A.;  
RL Submitted (OCT-1994) to the PIR data bank.  
DR PIR; PA0098; PA0098.  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1242 MW; 227BFCBA7C2772D7 CRC64;

Query Match 34.3%; Score 24; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.5e+03; Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPVEKLLPL 11  
:||| |  
Db 3 SPPVPKTFGL 12

## RESULT 14

Q8KPF2 PRELIMINARY; PRT; 16 AA.  
AC Q8KPF2; 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE Putative glycosyl transferase (Fragment).  
OS Clostridium perfringens.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1502;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=ATCC 10543;  
RX MEDLINE=22194081; PubMed=12204375;  
RA Calcutt M.J., Hsieh H.-Y., Chapman L.F., Smith D.S.;  
RT "Identification, molecular cloning and expression of an alpha-N-acetylglactosaminidase gene from Clostridium perfringens.";  
RL FEMS Microbiol. Lett. 214:77-80(2002).  
DR EMBL; AY121611; AAM55478.1; --  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Transferase.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1828 MW; C8C94354576B7B8F CRC64;

Query Match 34.3%; Score 24; DB 2; Length 16;

Best Local Similarity 27.3%; Pred. No. 4.8e+03; Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 PVEKLLPLSLK 14  
|::: |  
Db 6 PIDTWIKIELK 16

## RESULT 15

Q9QUY8 PRELIMINARY; PRT; 16 AA.  
ID Q9QUY8  
AC Q9QUY8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Histone H1 (Fragment).  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OC NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96070893; PubMed=7499230;  
 RA Gurley L.R., Valdez J.G., Buchanan J.S.;  
 RT "Characterization of the mitotic specific phosphorylation site of  
 RT histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B  
 RT kinase.";  
 RL J. Biol. Chem. 270:27653-27660(1995).  
 SQ SEQUENCE 16 AA; 1479 MW; 75EB488737288C8A CRC64;

Query Match 34.3%; Score 24; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPVEK 7  
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 Db 12 PPAEK 16

Search completed: October 27, 2004, 01:05:16  
 Job time : 139 secs





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: October 27, 2004, 09:22:01 ; Search time 30.5 Seconds  
(without alignments)  
4696.619 Million cell updates/sec

Title: US-09-980-881A-1\_COPY\_18\_1097  
Perfect score: 1932  
Sequence: 1 atgaagctttgcagcttgc.....ttttgcgcgtgtctctaaaa 1080

Scoring table:  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 478139 seqs, 66318000 residues  
Total number of hits satisfying chosen parameters: 956278

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1852.5	95.9	386	4	US-09-813-133A-2
2	1835	95.0	423	1	US-07-649-591B-3
3	1835	95.0	423	1	US-08-277-540-3
4	1835	95.0	423	1	US-08-430-787A-3
5	1835	95.0	423	2	US-08-869-057-2
6	1824	94.4	423	4	US-09-813-133A-4
7	640.5	33.2	404	1	US-08-696-139-2
8	639.5	33.1	415	2	US-08-860-882A-57
9	639.5	33.1	415	4	US-09-011-769A-39
10	638	33.0	417	1	US-07-649-591B-7
11	638	33.0	417	1	US-08-277-540-7
12	638	33.0	417	1	US-08-430-787A-7

13	635	32.9	417	1	US-07-649-591B-6
14	635	32.9	417	1	US-08-277-540-6
15	635	32.9	417	1	US-08-430-787A-6
16	635	32.9	417	4	US-09-917-254-66
17	632	32.7	424	4	US-09-011-769A-56
18	623	32.2	716	3	US-09-171-945-125
19	613.5	31.8	437	4	US-09-675-305-10
20	613.5	31.8	437	4	US-10-200-344-10
21	604	31.3	307	2	US-08-782-760-6
22	604	31.3	307	5	PCT-US96-00995-6
23	603.5	31.2	396	1	US-07-649-591B-4
24	603.5	31.2	396	1	US-08-277-540-4
25	603.5	31.2	396	1	US-08-430-787A-4
26	576	29.8	306	1	US-08-696-139-4
27	561	29.0	329	4	US-09-011-769A-51
28	561	29.0	349	4	US-09-011-769A-47
29	560	29.0	613	3	US-09-171-945-113
30	554	28.7	349	4	US-09-011-769A-60
31	553	28.6	349	4	US-09-011-769A-64
32	553	28.6	417	1	US-07-649-591B-8
33	553	28.6	417	1	US-08-277-540-8
34	553	28.6	417	1	US-08-430-787A-8
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36	546	28.3	399	4	US-10-200-910-8
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39	528.5	27.4	419	1	US-07-649-591B-5
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43	519.5	26.9	436	4	US-10-200-910-6
44	513	26.6	417	3	US-08-640-906-4
45	513	26.6	417	3	US-09-395-936-4

ALIGNMENTS

RESULT 1

US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Alignment Scores:  
Pred. No.: 2.09e-208 Length: 386  
Score: 1852.50 Matches: 354  
Percent Similarity: 94.16% Conservative: 1  
Best Local Similarity: 93.90% Mismatches: 5  
Query Match: 95.89% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-09-813-133A-2 (1-386)

QY	1	ATCAAGCTTTGCAGCTTCGAGTCCTTGACCATTTCTCTTCTGTGACGACGATGC	60
Db	1	MeCysSueCySerLeuValLeuValProIleValPheCysGluGlnHieVal	20
QY	61	TTTCGCTTCCAGAGTGGCCAAAGTCTTAGTCTTCTTAGAACCTCTAGGCAAGTTCAA	120





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QY 421 CCTGATATGCTTACAAAATCCACATTCGATCTCTATTTGAGAACTACCCACTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAAGGTTTCTGGAAGAAAGACAAACAGCCAAAATGCCATATGATGATTCGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATGCCAGAAATGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACAAATCATTCGATCGGAACAGACCTCGAATAGCACTTTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCAAAACACTGTGTGAGGAAGCTGCATCCAGTTCTCTCATGCTCGAAACCTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTGAGTTCAGAACCAAGTGAAGGAGGCTGAGTGTCTTCTGAGGAAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 300
QY 790 AACCAAGATTAAGCATATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCTATACAGCAAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAAATAGTAAATACCAATACCAATACCAATACCAATACCAATAC 969
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGCTCTGAGTGGGAGCAAGTGGGAGCAAGTGGGAGCAAGTGGGAGCA 1029
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QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
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Db 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

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RESULT 4

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US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-430-787A-3

Alignment Scores:
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Score: 1835.00 Matches: 356
Percent Similarity: 86.23% Conservative: 1
Best Local Similarity: 85.99% Mismatches: 3
Query Match: 94.98% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-430-787A-3 (1-423)

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Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTATACAAATATAGATGTTGTTCTCTGCGACGCCGTTACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTCAAGAAAACAACTCCATTTTGTAAATGCATCTCTGATGTCGACAAATGTG 240
Db 61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTCTGCGCAGAGCTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTCCAAACAGACAGTACAGCCCGGAGCCCTCGCATCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTTTATACTGAGAGGCAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCACATTCGATCTCTCTATTTGAGAACTACCCACTCTATGTT 480

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QY 541 CATGCCAGAGATGGATCTCTCTGTTTCTGCTTGTGTTTCATAGGCAT----- 591  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200  
QY 591 ----- 591  
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220  
QY 592 -----AATCGAATGTGGAAAG 609  
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240  
QY 610 AACCGTTCTTCTATGCGAACCAATCATTCGATCGGAACAGACCTCAATAGCAACTTGTGC 669  
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
QY 670 TCCAAACACTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACACTTACTGTGGA 729  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280  
QY 730 CTTTATCTGAGTCAGAACCAAGTGAAGGAGTGGCTAGTTTCTTGTGAGGAATAATATC 789  
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300  
QY 790 AACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 849  
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320  
QY 850 TCTTATACAGAAAGTAAAGCAAGACCATGAGGAAGTCTCTCTAGTACCCAGTGAAGCA 909  
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340  
QY 910 GTTCGTCTATTGACAAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 969  
Db 341 ValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360  
QY 970 ACCTTATACCTAGCTCCTGGAGTGGGACGATCGATCGATCTATGTTTGGGCATCAATAT 1029  
Db 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyr 380  
QY 1030 TCGTT-----TAC 1037  
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400  
QY 1038 ATCAAAACCCACTGTAGAGAAGCTTTGCCGCTGTCTCTAA 1079  
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 6

US-09-813-133A-4  
; Sequence 4, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-4  
Alignment Scores:  
Pred. No.: 4,876-205 Length: 423  
Score: 1824.00 Matches: 354  
Percent Similarity: 85.75% Conservative: 1

Best Local Similarity: 85.51% Mismatches: 5  
Query Match: 94.41% Indels: 55  
DB: 4 Gaps: 2  
US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-09-813-133A-4 (1-423)  
QY 1 ATGAAGCTTTTCAGCGCTTGAGTCTCTGTATCCCATTTGTTCTTCTGTGAGCAGCATGTC 60  
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
QY 61 TTCGCGTTCAGAGTGGCCAAAGTTCTAGCTGCTTCTCTAGAACCTCTAGCAAGTTCAA 120  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 121 GTTCTACAGATCTTACTACACATATGAGATTTCTTCTCGCAGCCGGTAAACAGCTCAC 180  
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTCTAAATGCATCTGATGTGCAAAATGTG 240  
Db 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
QY 241 AAAGCCATTAAATGTAGCGGAATTCATGCAAGTGTCTGTGGCAGAGCTGGAAGAT 300  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTTCCACGACACAGTCAAGCCCGAGGCTCGGCATCGTACTAT 360  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGATTTATACTAGAGAGCAT 420  
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
QY 421 CCTGATATGCTTACAAAAATCCACATTTGCATCTTCTAGAGAGTACCCACTCTATGTT 480  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
QY 481 TTAAGGTTTCTGAAAAGACAAACAGCCAAAATGCCATATGATGATGCTGGAATC 540  
Db 161 LeuLysValSerGlyLysGluGlnAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
QY 541 CATCCAGAGATGGATCTCTCTGCTTCTCTGCTGTGTGTTTCATAGGCCAT----- 591  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200  
QY 591 ----- 591  
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220  
QY 592 -----AATCGAATGTGGAAAG 609  
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240  
QY 610 AACCGTTCTTCTATGCGAACCAATCATTCGATCGGAACAGACCTGAATAGCAACTTGTGC 669  
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
QY 670 TCCAAACACTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACACTTACTGTGGA 729  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280  
QY 730 CTTTATCTGAGTCAGAACCAAGTGAAGGAGTGGCTAGTTTCTTGTGAGGAATAATATC 789  
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300  
QY 790 AACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 849  
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320  
QY 850 TCTTATACAGAAAGTAAAGCAAGACCATGAGGAAGTCTCTCTAGTACCCAGTGAAGCA 909  
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340

QY 910 GTTCGTGCTATTGACAAAACCTAGTAAATACCAAGTATACATGGCCATGGCTCAGAA 969  
 DB 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360  
 QY 970 ACCTTATACCTAGCTCTCGAGTGGGACGATTTGGATCTATGATTTGGCATCAATAT 1029  
 DB 361 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380  
 QY 1030 TCGTT-----TAC 1037  
 DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400  
 QY 1038 ATCAACCCACCTGTAGAAAGCTTTGGCGTGTCTCTAAA 1079  
 DB 401 IleLysProThrCysArgGluAlaPheAlaAlaValSerLys 414

RESULT 7

US-08-696-139-2  
 ; Sequence 2, Application US/08696139  
 ; Patent No. 5672496  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fayerman, Jeffrey T.  
 ; APPLICANT: Greenen, David P.  
 ; APPLICANT: Hershenberger, Charles L.  
 ; APPLICANT: Larson, Jeffrey L.  
 ; APPLICANT: Sterner, Jane L.  
 ; APPLICANT: Zhang, Haichao  
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Eli Lilly and Company  
 ; STREET: Lilly Corporate Center  
 ; CITY: Indianapolis  
 ; STATE: Indiana  
 ; COUNTRY: United States of America  
 ; ZIP: 46285

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/696,139  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/153,258  
 FILING DATE: 16-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-8681  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 404 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-696-139-2

Alignment Scores:  
 Pred. No.: 4,426-66  
 Score: 640.50  
 Percent Similarity: 54.29%  
 Best Local Similarity: 37.67%  
 Query Match: 33.15%  
 DB: 1  
 Length: 404  
 Matches: 136  
 Conservative: 60  
 Mismatches: 122  
 Indels: 43  
 Gaps: 6

US-09-980-881a-1\_COPY\_18\_1097 (1-1080) x US-08-696-139-2 (1-404)  
 QY 67 TTCAGAGTGGCCAGTTCTAGTGTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTTA 126  
 DB 10 PheGluGlyGluLysValPheArgValAsnValGluAspGluAsnAspIleSerLeuLeu 29  
 QY 127 CAGAATCTTACTCAACATATGAGATTTCTCTGGCAGCCGGTAAACAGTGCACCTTAT 186  
 DB 30 HisGluLeuAlaSerThrArgGlnIleAspPheTrpLysProAspSerValThrGlnIle 49  
 QY 187 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTGCACAATGTGAAAGCC 246  
 DB 50 LysProHisSerThrValAspPheArgValLysAlaGluAspIleLeuAlaValGluAsp 69  
 QY 247 CATTTAATGTGAGCGGAATTCATGCAGTGTCTGTGGCAGACGCTGGAAGATCTTATT 306  
 DB 70 PheLeuGluGlnAsnGluLeuGlnTyrGluValLeuIleAsnAsnLeuArgSerValLeu 89  
 QY 307 CAACAGCAGATTTCACACGACACAGTCCAGCCCCGAGCTCCGGCATCTGATCTATGAACAG 366  
 DB 90 GluAlaGlnPheAspSerArgVal-----ArgThrThrGlyHisSerTyrGluLys 106  
 QY 367 TATCACTCACTAATGAAATCTATCTTGGATAGATTTATAACTGAGAGGCATCTCAT 426  
 DB 107 TyrAsnAsnTrpGluThrIleGluAlaTrpThrLysGlnValThrSerGluAsnProasp 126  
 QY 427 ATGCTTACAAAAATCCACATGGATCCCTCATTTGAGAAAGTACCCACTCTATCTTTAAAG 486  
 DB 127 LeuIleSerArgThrAlaIleGlyThrThrPheLeuGlyAsnAsnIleTyrLeuLeuLys 146  
 QY 487 GTTCTGGAAGAAACAAACAGCCAAAATGCCATATGCCATATGATGATGCGAATCATGCC 546  
 DB 147 Val---GlyLysProGlyProAsnLysProAlaIlePheMetAspCysGlyPheHisAla 165  
 QY 547 AGAAGATGATCT 585  
 DB 166 ArgGluTrpIleSerHisAlaPheCysGlnTrpPheValArgGluAlaValLeuThrTyr 185  
 QY 585 ----- 585  
 DB 186 GlyTyrGluSerHisMetThrGluPheLeuAsnLysLeuAspPheTyrValLeuProVal 205  
 QY 586 -----GGCCAT-----AATCGAATGTGGAGAAAGAACCGT 615  
 DB 206 LeuAsnIleAspGlyTyrIleTyrThrTrpThrLysAsnArgMetTrpArgLysThrArg 225  
 QY 616 TCTTTCTATGCAACAAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGCTCCAAA 675  
 DB 226 SerThrAsnAlaGlyThrThrCysIleGlyThrAspProAsnArgAsnPhe---AspAla 244  
 QY 676 CACTGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGAAACCTACTGTGACTTTAT 735  
 DB 245 GlyTyrCysThrThrGlyAlaSerThrAspProCysAspGluThrTyrCysGlySerAla 264  
 QY 736 CCTGAGTCAGAACCAAGTGAAGCAGTGGTGTCTTCTGAGAGAAATATCAACCCAG 795  
 DB 265 AlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnAsnLeuSerSer 284  
 QY 796 ATTAAGCATATCATCAGCATGATCTATCTCCAGCATATAGTGTCTTCATATCTCTAT 855  
 DB 285 IleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetIleLeuTyrProTyrSerTyr 304  
 QY 856 ACAGGAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCAGTTCGT 915  
 DB 305 AspTyrLysLeuProGluAsnAsnAlaGluLeuAsnAsnLeuAlaLysAlaValLys 324  
 QY 916 GCTATTGACAAAACCTAGTAAATAACAGGTATACATGGCCATGGCTCAGAAACCTTA 975  
 DB 325 GluLeu---AlaThrLeuTyrGlyThrLysTyrThrTyrGlyProGlyAlaThrThrIle 343  
 QY 976 TACCTAGTCTCTGGAGTGGGAGCAGATTGATGATCTATGATTTGGGCATCAATATTCGTT 1035  
 DB 344 TyrProAlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleLysTyrSerPhe 363



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QY 1036 ACA 1038
Db 364 Thr 364

RESULT 8
US-08-860-882A-57
; Sequence 57, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGLESE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HOW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-882A-57

Alignment Scores:
Pred. No.: 5,87e-66 Length: 415
Score: 639.50 Matches: 140
Percent Similarity: 51.72% Conservative: 71
Best Local Similarity: 34.31% Mismatches: 136
Query Match: 33.10% Indels: 62
DB: 2 Gaps: 8

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-860-882A-57 (1-415)
QY 16 CTTGAGCTCTGTACCCATTGTTCTTCTGTGAGCAGCATGCTTCTTCGCG---TTCCAG 72
Db 2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisHisGlyGlyGluHisPheGlu 21
QY 73 AGTGCCAAAGTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAA 132
Db 22 GlyGluLysValPheArgValAsnValGluAspGluAsnHisIleAsnIleIleArgGlu 41
QY 133 CTTACTACACATATGAGATTGTTCTCTGCGCCGGTAAACAGCTCACCTTATTGTGAAG 192

Db 42 LeuAlaSerThrThrGlnIleAspPheThrLysProAspSerValThrGlnIleLysPro 61
QY 193 AAAAACAAGTCCATTTTGTAAATGCACTCTGATGTCGACAATGTGAAGAGCCCATTTA 252
Db 62 HisSerThrValAspPheArgValLysAlaGluAspThrValThrValGluAsnValLeu 81
QY 253 AATGTGAGCGGAATTCATGCAAGTCTTGTGTCGACAGCGTGAAGATCTTATTCAACAG 312
Db 82 LysGlnAsnGluLeuGlnTyrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101
QY 313 CAGATTTTCCAAACGACACAGTCAGCCCGACCTCCGCATCGTACTATGAACAGTATCAC 372
Db 102 GlnPheAspSerArgVal-----ArgAlaThrGlyHisSerTyrGluLysTyrAsn 118
QY 373 TCACTAAATGAAATCTATTCTTGATAGAAATTTATAACTGAGAGCGCATCTGTATGCTT 432
Db 119 LysTrpGluThrIleGluAlaTrpThrGlnValAlaThrGluAsnProAlaLeuIle 138
QY 433 ACAAAATCCACATTTGATCTCATTTTTCAGAGTACCCACTCTATGTTTAAAGTTTCT 492
Db 139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyrLeuLeuLysVal 157
QY 493 GGAAGAAGAAACAAACAGCCCAAAATGCCATATGATGATGATGATGATGATGATGATG 552
Db 158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisAlaArgGlu 177
QY 553 TGGATCTCTCTGCTTCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
Db 178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrGlyArg 197
QY 585 ----- 585
Db 198 GluIleGlnValThrGluLeuLeuAspLysLeuAspPheTyrValLeuProValLeuAsn 217
QY 586 -----GGCCAT-----AATCGAATGTGAGAAAGAACCGTCTTCTTTC 621
Db 218 IleAspGlyTyrIleTyrThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237
QY 622 TATCGCAACAATCATTTGATCGAAGACAGCTGATGATGATGATGATGATGATGATGATG 681
Db 238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTyr 256
QY 682 TGTGAGGAAGTGCATCCAGTTCCTCATGTCGGAACCTACTGTGGAATTTATCCTCAG 741
Db 257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrCysGlyProAlaAlaGlu 276
QY 742 TCAGAACCAAGTGAAGCAGTGGCTAGTTTCTTGAAGAAATATCAACAGATTAATA 801
Db 277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296
QY 802 GCATATCATGACATGATTCATCTCCAGCATATAGTGTTCATATTCCTATACACAGA 861
Db 297 AlaTyrLeuThrIleHisSerTyrSerGlnMetIleTyrProTyrSerTyrAlaTyr 316
QY 862 AGTAAACCAAGACCATGAGAACTGCTCTAGTACGACGAGTTCGTGCTATT 921
Db 317 LysLeuGlyGluAsnAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336
QY 922 GACAAATCTAGTAAATAATACCAAGGTATACACATGGCATGGCTCAGAACCTTATACCTA 981
Db 337 ---AlaSerLeuHisGlyThrLysTyrThrTyrGlyProGlyAlaThrThrIleTyrPro 355
QY 982 GCTCTGAGGTGGGACGATGATCTATGATTTGGGCATCAATATTCGTTTACATC- 1040
Db 356 AlaAlaGlyGlySerAspAspTrpAlaTyrAspGlnGlyIleArgTyrSerPheThrPhe 375
QY 1041 -----AAACCCACC 1049
Db 376 GluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluSerGlnIleArgAlaThr 395
QY 1050 TGTAGAGAGCTTTTTCGCGCTGTC 1073
Db 1050 TGTAGAGAGCTTTTTCGCGCTGTC 1073
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Db 396 CysGluGluThrPheLeuAlaIle 403

RESULT 9

US-09-011-769A-39

Sequence 39, Application US/09011769A

Patent No. 6436691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKE, David C.

DAVIES, David H.

HENNAM, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 415 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-011-769A-39

Alignment Scores:

Pred. No.: 5.87e-66 Length: 415

Score: 639.50 Matches: 140

Percent Similarity: 51.72% Conservative: 71

Best Local Similarity: 34.31% Mismatches: 136

Query Match: 33.10% Indels: 62

DB: 4 Gaps: 8

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-09-011-769A-39 (1-415)

QY 16 CTTGACGCTCTGTACCATGTCTCTCTGTGAGCAGCATCTCTCGG---TTCCAG 72

Db 2 LeuLeuValLeuValThrValAlaLeuAlaSerAlaHisGlyGlyGluHisPheGlu 21

QY 73 AGTGGCCAACTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTACAGAA 132

Db 22 GlyGluValPheArgValAsnValGluAsnHisIleAlaArgGlu 41

QY 133 CTTACTACAAATATAGATGTCTCTGCGACCGGTAAACAGCTGACCTTATGTGAAG 192

Db 42 LeuAlaSerThrThrGlnIleAspPheThrLysProAspSerValThrGlnIleLysPro 61

QY 193 AAAAACAAGTCCATTTTTTTGTAATGCATCTGATGCGACAATGTGAAAGCCCATTTA 252

Db 62 HisSerThrValAspPheArgValAsnValGluAsnValLeuValLeuValLeu 81

QY 253 AATGTGACCGGAATTCATGAGTGTCTGTGCGACAGCTGGAAGATCTTATTCAACAG 312

Db 82 LysGlnAsnGluLeuGlnThrLysValLeuIleSerAsnLeuArgAsnValValGluAla 101

QY 313 CAGATTTCCAAACGACACAGTCAGCCCGAGCTCCGCATCGTACTATGAAACAGTATCAC 372

Db 102 GlnPheAspSerArgVal-----ArgAlaThrGlyHisSerThrGluLysThrAsn 118

QY 373 TCATTAATGAATCTATTCTTGGATAGAAATTTATACTGAGAGCATCTCTGATATGCTT 432

Db 119 LysTrpGluThrIleGluAlaThrGlnGlnValAlaThrGluAsnProAlaLeuIle 138

QY 433 ACAAAAATCCACATTTGGATCTCTATTTGAGAAGTACCCACATCTATGTTTAAAGTTTCT 492

Db 139 SerArgSerValIleGlyThrThrPheGluGlyArgAlaIleTyLeuLeuLysVal--- 157

QY 493 GGAAGAAACAAACAGCCCAAAATGCCATATGCTGATTTGATGCTGGAAATCCATCCAGAGAA 552

Db 158 GlyLysAlaGlyGlnAsnLysProAlaIlePheMetAspCysGlyPheHisalaArgGlu 177

QY 553 TGGATCTCTCTGCTTTCTGCTTGTGTTCTATA----- 585

Db 178 TrpIleSerProAlaPheCysGlnTrpPheValArgGluAlaValArgThrTyrglyArg 197

QY 585 ----- 585

Db 198 GluIleGlnValThrGluLeuAspLysLeuAspPheTyrglyValLeuProValLeuAsn 217

QY 586 -----GGCCAT-----AATCCAATGTGGAAGAAACCGTTCTTTTC 621

Db 218 IleAspGlyTyrlleTyrlleThrTrpThrLysSerArgPheTrpArgLysThrArgSerThr 237

QY 622 TATGCAACAATCATTGTCATCGGAACAGACCTGAATAGCACTTGTCTCCAAACACTGG 581

Db 238 HisThrGlySerSerCysIleGlyThrAspProAsnArgAsnPhe---AspAlaGlyTrp 256

QY 682 TGTGAGGAGGTGCATCCAGTTCTCTGCGAACCTACTGCGACTTATCTATCTGCTGAG 741

Db 257 CysGluIleGlyAlaSerArgAsnProCysAspGluThrTyrglyProAlaalaGlu 276

QY 742 TCAGAACCAAGAGTGAAGCGCTAGTCTTTCTGAGAAGAAATATCAACAGATATAA 801

Db 277 SerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnLysLeuSerSerIleLys 296

QY 802 GCATACATCAGCATGCTATCTACTCCAGCATATAGTGTCTTCCATATCTATATACAGA 861

Db 297 AlaTyrlleThrIleHisSerTyrglyMetIleTyrglyProTyrglySerTyrglyAla 316

QY 862 AGTAAAGCAAGACCATGAGCACTGCTCTAGTAGCCAGTCAGTGAAGCAGTCTGCTATT 921

Db 317 LysLeuGlyGluAsnAlaGluLeuAsnAlaLeuAlaLysAlaThrValLysGluLeu 336

QY 922 GACAAACTAGTAAAAATACAGGTATACACATGCGCATGCGTCCAGAAACCTTATACCTA 981

Db 337 ---AlaSerLeuHisGlyThrLysTyrlleTyrglyProGlyAlaThrThrIleTyrgly 355

QY 982 GCTCTGAGGAGTGGGACGATGATCTATGATTTGGCATCAAAATTCGTTTACATC- 1040

Db 356 AlaAlaGlyGlySerAspAspTrpAlaTyrglyGlnGlyIleArgTyrglySerPheThr 375

QY 1041 -----AAACCCACC 1049

Db 376 GluLeuArgAspThrGlyArgTyrglyPheLeuLeuProGluSerGlnIleArgAlaThr 395

QY 1050 TGTAGAGAGCTTTTCCCGCTGTC 1073

Db 396 CysGluGluThrPheLeuAlaIle 403

RESULT 10

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US-07-649-591B-7
; Sequence 7, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; CITY: 460 Point San Bruno Blvd
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-649-591B-7

Alignment Scores:
Pred. No.:      Length:      417
Score:          638.00      Matches:      147
Percent Similarity: 51.23%      Conservative: 62
Best Local Similarity: 36.03%      Mismatches:   135
Query Match:      33.02%      Indels:       65
DB:               1          Gaps:         9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-07-649-591B-7 (1-417)
QY 16 CTGCGAGTCTGTACCCATTGCTCTCTCTGTGAGCAGCATGCTTCGCGTTCAGAGT 75
Db 7 MetAlaValIleTyr-ThrThrLeuAlaIleAlaProValHis-----PheAspArg 23
QY 76 GGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTCTTACAGATCTT 135
Db 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43
QY 136 ACTACACATAGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTATTGTGAAGAAA 195
Db 44 ThrGlnSerIleGluLeuAspPheTrpTyrProAspAlaIleHisAspIleAlaValAsn 63
QY 196 AAACAAGTCCATTTTTTTGTAATGCATCTGTGACAAATGTGAAAGCCCATTTAAAT 255
Db 64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83
QY 256 GTGACGGGAATCCATGCAGTCTCTGTGGCAGAGCTGGAAGTCTTATTCACAGCAG 315
Db 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluGluLysGln 103
QY 316 ATTTC---AAGCACACAGTCCAGCCCGAGCCTCGCATCTGTATGACAGATATCAC 372
Db 316 ATTTC---AAGCACACAGTCCAGCCCGAGCCTCGCATCTGTATGACAGATATCAC 372

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CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,540  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Haeak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-277-540-7

Alignment Scores:  
Pred. No.: 8,83e-66 Length: 417  
Score: 638.00 Matches: 147  
Percent Similarity: 51.23% Conservative: 62  
Best Local Similarity: 36.03% Mismatches: 135  
Query Match: 33.02% Indels: 65  
DB: 1 Gaps: 9

US-09-980-881a-1\_copy\_18\_1097 (1-1080) x US-08-277-540-7 (1-417)

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QY 16 CTTGAGCTCTGTACCCATTGTTCTCTGTGAGCAGCATGCTTTCGGCTTCAGAGT 75
   ::::::::::: ::::
Db 7 MetAlaValIleTyrThrLeuAlaIleAlaProValHis-----PheAspArg 23

QY 76 GGCCAAAGTTCTAGCTGCTCTCTCCAGAACCTTAGGCAAGTTCAGATTCACAGATCTT 135
   ::::::::::: ::::
Db 24 GluLysValPheArgValLysLeuGlnAsnGluLysHisAlaSerValLeuLysAsnLeu 43

QY 136 ACTACACATATGAGATGTTCTCTGCACCGGTAAACAGCTGACCTTATTGGAAGAAA 195
   ::::::::::: ::::
Db 44 ThrGlnSerIleGluLeuAspPheTyrPyrProAspAlaIleHisAspIleAlaValAsn 63

QY 196 AAACAAGTCCATTTTTTTGTAATATGTCATCTGACATTCGACAAATGTGAAGCCCATTTAAAT 255
   ::::::::::: ::::
Db 64 MetThrValAspPheArgValSerGluLysGluSerGlnThrIleGlnSerThrLeuGlu 83

QY 256 GTGAGCCGAATTCATCAGTGTCTCTGCGCAGACCTGGAAGATCTTATTCACAGCAG 315
   ::::::::::: ::::
Db 84 GlnHisLysIleHisTyrGluIleLeuIleHisAspLeuGlnGluIleGluLysGln 103

QY 316 ATTTC---AACGACACAGTCCCGGAGCTCCGCATCGTACTATGAACAGTATCAC 372
   ::::::::::: ::::
Db 104 PheAspValLysAspGluIleAlaGlyArgHisSer-----TyrAlaLysTyrAsn 120

QY 373 TCACATAAGAAATCTATTCTTGGATAGAATTTATACTGAGAGGCATCTGATATGCTT 432
   ::::::::::: ::::
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Db 121 AspTrpAspLysIleValSerTrpThrGluLysMetLeuGluLysHisProGluMetVal 140
QY 433 ACAAAATCCACATTTGGATCTCTATTCAGAGAGTACCCACTCTATGTTTAAAGTTTCT 492
   ::::::::::: ::::
Db 141 SerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeuLysIle--- 159
QY 493 GGAAAGAACAAACAGCCCAAAATATGCTATGATGATGCTGTTGGAATCCATCCAGAGAA 552
   ::::::::::: ::::
Db 160 GlyLysLysAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu 179
QY 553 TGGATCTCTCTGCTTCTTCTGTTGGTTTCATA-----GGCCAT 591
   ::::::::::: ::::
Db 180 TrpIleSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysSerTyrGlyLys 199
QY 592 RAT----- 594
   ::::
Db 200 AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrValLeuProValPheAsn 219
QY 595 -----CGAATGTGGAGAAAGAACCGTCTTCTTTC 621
   ::::::::::: ::::
Db 220 ValAspGlyTyrIleTrpSerTrpThrGlnAspArgMetTrpArgLysAsnArgSerArg 239
QY 622 TATGCAACAATCATTCGGAACAGACCTGAATAGCAACTTGTCTCCAAACACTCG 681
   ::::::::::: ::::
Db 240 AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp 258
QY 682 TGTGAGGAAGGTGCATCCAGTCTCCTCGAAACCTACTGTGGACTTTTATCTCTAG 741
   ::::::::::: ::::
Db 259 AspSerSerProAsnThrAsnLysProCysLeuAsnValTyrArgGlyProAlaProGlu 278
QY 742 TCAGAACCCAGAGTGAAGCAGTGTCTTCTTGGAGAGAAATATCAACAGATATAA 801
   ::::::::::: ::::
Db 279 SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys 298
QY 802 GCATCATCAGCATGATTCATCTACCTCCAGCATATAGTGTTCATATTCCTATACACGA 861
   ::::::::::: ::::
Db 299 AlaTyrIlePheHisSerTyrSerGlnMetLeuLeuIleProTyrGlyTyrThrPhe 318
QY 862 ACTAAAGCAAGACCATGAGCACTGTCTCTAGTAGCCAGTGAACAGTTCGTGCTATT 921
   ::::::::::: ::::
Db 319 LysLeuProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu 338
QY 922 GACAAACTAGTAAAAATACCAAGGTATACATGCGCATGGCTCAGAAAACCTTATACCTA 981
   ::::::::::: ::::
Db 339 ---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleAlaSerThrIleTyrLys 357
QY 982 GCTCTGAGAGGTGGGACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
   ::::::::::: ::::
Db 358 ThrSerGlySerSerLeuAspTrpValTyrAspLeuGlyLysHisThrPheAlaPhe 377
QY 1038 -----ATCAAAACCCACC 1049
   ::::::::::: ::::
Db 378 GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProThr 397
QY 1050 TGTAGAGAGAGCTTTTCCCGCTGTC 1073
   ::::::::::: ::::
Db 398 CysLysGluThrMetLeuSerVal 405
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RESULT 12
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
```

QY	433	ACAAAATCCACATTCGATCCTCATTTGAGAACTACCCACTCTATGTTTAAAGGTTTCT	493
DB	141	SerArgLeuIleGlySerThrValGluAspAsnProLeuIleValleuysile---	159
QY	493	GGAAAAGAACAAACAGCCAAAATATGCCATATGCAATGCACTGTGGAATCCATGCCAGAA	552
DB	160	GlyIleAspGlyGluArgLysAlaIlePheMetAspCysGlyIleHisAlaArgGlu	179
QY	553	TGGATCTCTCCTGCTTTCCTGCTTGTGGTTTCATA-----GGCAT	591
DB	180	TrpIleSerProAlaPheCysGlnTrpPheValIleGlnAlaThrLysSerTyArgLys	199
QY	592	AAT-----	594
DB	200	AsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyValLeuProValPheAsn	219
QY	595	-----CGAATGTGGAGAAAGAACCGTTCTTTC	621
DB	220	ValAspGlyTyIleTrpSerThrGlnAspArgMetTrpArgLysAsnArgSerArg	239
QY	622	TATGCGNACAATCATTCGATCGAAGCAGACTGATAGCAACTTGTCTCCAAACACTGG	681
DB	240	AsnGlnAsnSerThrCysIleGlyThrAspLeuAsnArgAsnPhe---AspValSerTrp	258
QY	682	TGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGCACTTTATCCTCGAG	741
DB	259	AspSerSerProAsnThrAsnLysProCysLeuAsnValTyArgGlyProAlaProGlu	278
QY	742	TCGAACCAAGAGTGAAGGAGTGGCTAGTTCTTTGAGAAAGAATATCAACCAGATTAAA	801
DB	279	SerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsnSerIleLys	298
QY	802	GCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCCATATTCCTATACACGA	861
DB	299	AlaTyIleThrPheHisSerTySerGlnMetLeuLeuIleProTyArgTyThrPhe	318
QY	862	AGTAAAGCAAGACCATGAGGAACCTGCTCTCTAGTAGCCAGTAGAAGCAGTTCTGCTATT	921
DB	319	LysLeuProProAsnHisGlnAspLeuLeuLysValAlaArgIleAlaThrAspAlaLeu	338
QY	922	GACAAACTAGTAAANAATACAGGTATACATGGCCCATGGCTCAGAAACCTTATACCTA	981
DB	339	---SerThrArgTyArgGluThrArgTyIleTyArgTyProIleAlaSerThrIleTyLys	357
QY	982	GCTCCTGGAGGTGGGACGATTCGATCTATGATTGGGCATCAATATTCGTTTAC----	1037
DB	358	ThrSerGlySerSerLeuAspTrpValTyAspLeuGlyIleLysHisThrPheAlaPhe	377
QY	1038	-----ATCAACCCACC	1049
DB	378	GluLeuArgAspLysGlyLysSerGlyPheLeuLeuProGluSerArgIleLysProthr	397
QY	1050	TGTAGAGAAGCTTTTGGCGGTGC	1073
DB	398	CysLysGluThrMetLeuSerVal	405

RESULT 13  
 US-07-649-5918-6  
 ; Sequence 6, Application US/07649591B  
 ; Patent No. 5206161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis Drayna and Daniel Eaton  
 ; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-6

Alignment Scores:
Pred. No.: 1,99e-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: 1 Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-07-649-591B-6 (1-417)

QY 16 CTTGCAGTCCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTCCTTCGCCG----- 66
DB 1 MetArgLeuLeuLeuProValGlyLeuIleAlaThrLeuAlaIleAlaProValArg 20

QY 67 TTCCAGAGTGGCCAGTCTTCTAGCTGCTCTTCTCTAGAACCTCTAGGCAAGTTCAGATTCTA 126
DB 21 PheAspArgGluLysValPheArgValLysProGlnAspGluLysGlnAlaAspIleIle 40

QY 127 CAGATCTTACTACACATATGAGATTGTTCTCTGCGACGCCGTAACACCTGACCTATT 186
DB 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrProGlyAlaThrHisVal 60

QY 187 GTGAGAAAAACAAGTCCATTTTGTGTAATGTCATCTGTGACAACTGTGAAAGCC 246
DB 61 AlaAlaAsnMetMetValAspPheArgValSerGluLysGluSerGlnAlaIleGlnSer 80

QY 247 CATTAAATGTGAGCGGAATTCATCAGTGTCTCTGTCGACAGCTGGAAGATCTTATT 306
DB 81 AlaLeuAspGlnAsnLysMetHisTyrGluIleLeuIleHisAspLeuGlnGluIle 100

QY 307 CAACAGCAGATTTC---AACGACAGCTCAGCCCCGAGCCCTCCGATCGTACTATGAA 363
DB 101 GluLysGlnPheAspValLysGluAspIleProGlyArgHisSer-----TyrAla 117

QY 364 CAGTATCCTCACTAAATGAATTTCTTGTGATAGATTTATTAAGTGGAGGCATCCT 423
DB 118 LysTyrAsnAsnTrpGluLysIleValAlaIleThrGluLysMetMetAspLysTyrPro 137

QY 424 GATATGCTTACAAAAATCCACATTTGATCTCTCTTGTGAGAGTACCACCTCTATGTTTA 483
DB 138 GluMetValSerArgIleLysIleGlySerThrValGluAspAsnProLeuTyrValLeu 157

QY 484 AGGTTTCTGGAAAAACAAACAGCCAAATATGCCATATGGATTGACTGTGAAATCCAT 543
DB 158 LysIle---GlyGluLysAsnGluArgGlyAlaIlePheMetAspCysGlyIleHis 176

QY 544 GCCAGAGATGGATCTCTCTGCTTCTGCTTCTGTTGTTTCATA----- 585

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Db 177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196
QY 585 ----- 585

Db 197 TyrGlyArgAsnLysIleMetThrLysLeuLeuAspArgMetAsnPheTyrIleLeuPro 216
QY 586 -----GCCCAT-----AATCGAATGTGAGAAAGAAC 612
Db 217 ValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsnArgMetTrpArgLysAsn 236
QY 613 CGTTCTTCTTATGCGAACAATCATTCATCGGACAGACCTGAATAGCACTTCTCTCC 672
Db 237 ArgSerLysAsnGlnAsnSerLysCysIleGlyThrAspLeuAsnArgAsnPhe---Asn 255
QY 673 AACACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCTCGCGAACCTACTGTGGACTT 732
Db 256 AlaSerTrpAsnSerIleProAsnThrAsnAspProCysAlaAspAsnTyrArgGlySer 275
QY 733 TATCTGTAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTCTTCTTGTGAGAAATATCAAC 792
Db 276 AlaProGluSerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsn 295
QY 913 CGTGCTATTGACAAAACTAGTAAAAATACCAAGGTATACATGCGCATGGCTCAGAAACC 972
Db 336 AspValLeu---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleGluSerThr 354
QY 973 TTATACCTAGCTCTCTGAGGTGGGACCATGCGATGATGATTTGGCATCAATATTCG 1032
Db 355 IleTyrProIleSerGlySerSerLeuAspTrpAlaTyrAspLeuGlyIleLysHisThr 374
QY 1033 TTTAC-----ATC 1040
Db 375 PheAlaPheGluLeuArgAspLysGlyLysPheGlyPheLeuLeuProGluSerArgIle 394
QY 1041 AAACCCACCTGTAGAGAAAGCTTTTCCCGCTGTC 1073
Db 395 LysProThrCysArgGluThrMetLeuAlaVal 405

RESULT 14
US-08-277-540-6
; Sequence 6, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-277-540-6

Alignment Scores:
Pred. No.: 1,99e-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: 1 Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-277-540-6 (1-417)
QY 16 CTTCAGTCCTGTACCAATGTTCTCTCTGTGAGCAGCATGCTTCGCGG----- 66
DB 1 MetArgLeuLeuProValGlyLeuLeuAlaThrThrLeuAlaileAlaProValArg 20
QY 67 TTCAGAGTGGCAAGTCTAGCTCTCTCTAGCACTCTAGGCAAGTTCAGGTTCTA 126
DB 21 PheAspArgGluValPheArgValLysProGlnAspGluLysGlnAlaSpille 40
QY 127 CAGATCTTACTACACATATAGATGTTCTCTGCGACCGGTAACAGCTGACCTTAT 186
DB 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTyrProGlyAlaThrHisVal 60
QY 187 GTGAGAAAAACAGTCCATTTTCTTAATGTCATCTGATCGCAATGTGAAGCC 246
DB 61 AlaAlaAsnMetMetValAspPheArgValSerGluLysGluSerGlnAlaileGlnSer 80
QY 247 CATTTAAATGTGAGCGGAATTCATGCACTGTCTTGTGGCAGACGTGGAAGATCTTAT 306
DB 81 AlaLeuAspGlnAsnLysMethHisTyrGluLeuLeuLeuHisAspLeuGlnGluLeu 100
QY 307 CAACAGCAGATTCC---AACGACACAGTCAGCCCCCGAGCTCCGCATCGTACTATGAA 363
DB 101 GluLysGlnPheAspValLysGluAspPheProGlyArgHisSer-----TyrAla 117
QY 364 CAGTATCACTCAATAAGAAATCTTCTTGGATAGATTTATTAACCTGAGGCGATCCT 423
DB 118 LysTyrAsnAsnTrpGluLysileValAlaThrThrGluLysMetMetAspLysTyrPro 137
QY 424 GATATGCTTACAAAAACACATCTTGATCTCATTTGAGAGTACCCTCTATGTTTAA 483
DB 138 GluMetValSerArgLysileGlySerThrValGluAspAsnProLeuTyrValLeu 157
QY 484 AAGTTTCTGGAAGAAACAAACAGCCAAATATGATATGATGATGATGATGATGATGAT 543
DB 158 Lysile---GlyGluLysAsnGluArgArgLysAlailePheMetAspCysGlyileHis 176
QY 544 CCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 585
DB 177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196
QY 585 ----- 585

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Db 197 TyrGlyArgAsnLysileMetThrLysLeuLeuAspArgMetAsnPheTyrIleLeuPro 216
QY 586 -----GGCCAT-----AATCGAATGTGAGAAAGAAC 612
Db 217 ValPheAsnValAspGlyTyrIleTrpSerTrpThrLysAsnArgMetTrpArgLysAsn 236
QY 613 CGTTCTTTCTATGCGAAACAATCATTGTCATGGAACAGACCTGAATAGCAACTTTGTCTCC 672
Db 237 ArgSerLysAsnGlnAsnSerLysCysileGlyThrAspLeuAsnArgAsnPhe---Asn 255
QY 673 AAACACTGGTGTGAGGAAGGTGCATCCAGTTTCCTCTCTCGGAAACCTACTGTGGACTT 732
Db 256 AlaSerTrpAsnSerIleProAsnThrAsnAspProCysAlaAspAsnTyrArgGlySer 275
QY 733 TATCTGAGTCAGAACCAAGAGTGAAGCAGTGTAGTTCTTCTGAGAGAAATATCAAC 792
Db 276 AlaProGluSerGluLysGluThrLysAlaValThrAsnPheIleArgSerHisLeuAsn 295
QY 793 CAGATTAAAGCATACATCAGCATGCTTCTACTCTCCAGCATATAGTGTTCCTCATATTC 852
Db 296 GluLeuLysValTyrIleThrPheHisSerTyrSerGlnMetLeuLeuPheProTyrGly 315
QY 853 TATACAGAGTAAAGCAAGCAACATCAGGAACTGTCTTAGTAGCCAGTGAAGCAGTT 912
Db 316 TyrThrSerLysLeuProAsnHisGluAspLeuAlaLysValAlaLysileGlyThr 335
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Db 336 AspValLeu---SerThrArgTyrGluThrArgTyrIleTyrGlyProIleGluSerThr 354
QY 973 TTATACCTAGTCTCTGAGGTGGGAGCATGATGATGATGATGATGATGATGATGATGATG 1032
Db 355 IleTyrProLysSerGlySerSerLeuAspTrpAlaTyrAspLeuGlyIleLysHisThr 374
QY 1033 TTTAC-----ATC 1040
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QY 1041 AAACCCACCTGTAGAGAGCTTTTGGCGCTGTC 1073
Db 395 LysProThrCysArgGluThrMetLeuAlaVal 405

RESULT 15
US-08-430-787A-6
; Sequence 6, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674e1 Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944

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; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA: 07/649591
; APPLICATION NUMBER: 01-FEB-91
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-430-787A-6

Alignment Scores:
Pred. No.: 1,99e-65 Length: 417
Score: 635.00 Matches: 139
Percent Similarity: 52.31% Conservative: 76
Best Local Similarity: 33.82% Mismatches: 132
Query Match: 32.87% Indels: 65
DB: 9 Gaps: 9

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-08-430-787A-6 (1-417)

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QY 67 TTCAGAGTGGCAAGTTCTAGTCTCTCTGAGCACTCTAGCAAGTTCAAGTTCTA 126
Db 21 PheAspArgGluLysValPheArgValLysProGlnAspGluLysGlnAlaAspIle 40

QY 127 CAGAACTTCTACACATATGAGATTGTTCTCTGCGCGCGGTACACGCTGACCTATT 186
Db 41 LysAspLeuAlaLysThrAsnGluLeuAspPheTrpTyrProGlyAlaThrHisVal 60

QY 187 GTCAAGAAAAACAAGTCCATTTTGTAAATGCATCTGTCGACAAATGGAAGCC 246
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QY 247 CATTATAATGTGAGCGGAATTCATGCAAGTCTCTCTGCGCAGACGCGGAAGATCTTATT 306
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QY 307 CAACAGCAGATTTC---AACGACACAGTCAGCCCGCGAGCCTCCGCTACTATGAA 363
Db 101 GluLysGlnPheAspValLysGluAspIleProGlyArgHisSer-----TyrAla 117

QY 364 CAGTATCACTCACTAAATGAATCTTCTCTGATAGATTTATTAAGTGAAGGCATCT 423
Db 118 LysTyrAsnAsnTrpGluLysIleValAlaTrpThrGluLysMetMetAspLysTyrPro 137

QY 424 GATATGCTTACAAAAATCCATTGGATCTCTCTGAGAAAGTACCACCTCTATGTTTA 483
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QY 484 AAGTTTCTGGAAGAACAAACAGCCAAATGCCATATGGATTGACTGTGGAATCCAT 543
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QY 544 GCCAGAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 585
Db 177 AlaArgGluTrpValSerProAlaPheCysGlnTrpPheValTyrGlnAlaThrLysThr 196

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QY 673 AAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCATCTCGGAAACCTTACTGTGACTT 732
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QY 793 CAGATTAAGCATACATCAGCATGCAATTCATCTACTCCAGCATATAGTGTTCATATTC 852
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QY 853 TATACACGAAGTAAAGCAAGACCATGAGGAACGTCTCTAGTAGCCAGTCAAGCAGTT 912
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Search completed: October 27, 2004, 10:41:12
Job time : 43.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 27, 2004, 10:30:15 : Search time 535.5 Seconds  
(without alignments)  
1307.761 Million cell updates/sec

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Scoring table: BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 2741442

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO.spool\_p/US09980881/runat\_26102004\_084539\_8822/app\_query.fasta\_1.1223  
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-LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0  
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Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

Alignment Scores: 9.79e-184 Length: 386  
Pred. No.: 386

No.	Score	Match	Length	DB	ID	Description
1	1852.5	95.9	386	9	US-09-813-133A-2	Sequence 2, Appli
2	1852.5	95.9	386	14	US-10-212-877-2	Sequence 2, Appli
3	1835	95.0	423	14	US-10-379-836-17	Sequence 17, Appli
4	1824	94.4	423	9	US-09-813-133A-4	Sequence 4, Appli
5	1824	94.4	423	14	US-10-212-877-4	Sequence 4, Appli
6	1811.5	93.8	428	15	US-10-115-479-68	Sequence 68, Appli
7	1811.5	93.8	428	15	US-10-115-479-70	Sequence 70, Appli
8	1746	90.4	423	14	US-10-379-836-2	Sequence 2, Appli
9	1550.5	80.3	422	14	US-10-379-836-18	Sequence 18, Appli
10	1522.5	78.8	422	14	US-10-379-836-16	Sequence 16, Appli
11	1442.5	74.7	322	15	US-10-115-479-64	Sequence 64, Appli
12	1396.5	72.3	354	15	US-10-115-479-66	Sequence 66, Appli
13	839	43.4	211	9	US-09-925-302-467	Sequence 467, App
14	839	43.4	211	10	US-09-925-302-467	Sequence 467, App
15	646	33.4	416	15	US-10-074-978A-269	Sequence 269, App
16	641	33.2	417	15	US-10-074-978A-267	Sequence 267, App
17	641	33.2	417	15	US-10-074-978A-268	Sequence 268, App
18	641	33.2	417	16	US-10-477-515-3	Sequence 3, Appli
19	635	32.9	417	14	US-10-229-546-2	Sequence 2, Appli
20	635	32.9	417	14	US-10-229-546-9	Sequence 9, Appli
21	635	32.9	417	14	US-10-341-434-188	Sequence 188, App
22	635	32.9	417	15	US-10-282-511-72	Sequence 72, Appli
23	632	32.7	402	14	US-10-379-836-20	Sequence 20, Appli
24	627.5	32.5	416	15	US-10-074-978A-270	Sequence 270, App
25	623	32.2	716	9	US-09-910-059-125	Sequence 125, App
26	622	32.2	416	15	US-10-074-978A-266	Sequence 266, App
27	613.5	31.8	434	16	US-10-477-515-2	Sequence 2, Appli
28	613.5	31.8	437	13	US-10-200-344-10	Sequence 10, Appli
29	613.5	31.8	437	14	US-10-274-639-12	Sequence 12, Appli
30	613.5	31.8	437	15	US-10-333-574-12	Sequence 12, Appli
31	611.5	31.7	437	17	US-10-757-262-128	Sequence 128, App
32	564.5	29.2	374	9	US-09-888-615-61	Sequence 61, Appli
33	563	29.1	444	14	US-10-176-306-74	Sequence 74, Appli
34	560	29.0	613	9	US-09-910-059-113	Sequence 113, App
35	560	29.0	613	16	US-10-608-710-4	Sequence 4, Appli
36	546	28.3	399	14	US-10-200-910-8	Sequence 8, Appli
37	546	28.3	399	17	US-10-843-130-8	Sequence 8, Appli
38	533.5	27.6	419	15	US-10-072-012-788	Sequence 788, App
39	528.5	27.4	350	13	US-10-200-344-12	Sequence 12, Appli
40	524.5	27.1	286	16	US-10-408-765A-1959	Sequence 1959, Ap
41	522	26.9	286	15	US-10-072-012-887	Sequence 887, App
42	519.5	26.9	419	15	US-10-257-174-40	Sequence 40, Appli
43	519.5	26.9	436	14	US-10-200-910-6	Sequence 6, Appli
44	519.5	26.9	436	15	US-10-072-012-316	Sequence 316, App
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ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Score: 1852.50 Matches: 354  
Percent Similarity: 94.16% Conservative: 1  
Best Local Similarity: 93.90% Mismatches: 5  
Query Match: 95.89% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-09-813-133A-2 (1-386)

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DB 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
QY 61 TTCGGGTTCCAGAGTGGCCAACTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
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DB 41 ValLeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGCATCTGATGTCGACAATGTG 240  
DB 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
QY 241 AAAGCCCATTTAAATGTAGCGGAATTCATGACAGTCTTCTGCTGGCAGACGTGGAAGAT 300  
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTTCCAAACACACAGCAGTCCCGCCGAGCTCGCATCTGACTAT 360  
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrr 120  
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTGGATAGAAATTTATACTGAGAGGCAT 420  
DB 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHis 140  
QY 421 CCGTATATGCTTACAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCCACTCTATGT 480  
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QY 481 TTTAAAGGTTTCTGGAAAAAACAACAGCCAAAATGCCATATGATTGACTGTGGAATC 540  
DB 161 LeuLysValSerGlyLysGluGlnAlaLysAsnAlaIleTrpIleAspCysGlyIle 180  
QY 541 CATGCCAGAAATGAGATCTCTCTGCTGCTTCTGCTGCTGCTCATAGGCCAATATCAATG 600  
DB 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
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DB 201 TrpArgLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 220  
QY 661 AACTTTGTCTCCAAACACTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACC 720  
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QY 781 AGAAATATCAACAGATTAAAGCATATCATCATGCTATCTACTCCAGCATATAGT 840  
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; Sequence 2, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO011173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-212-877-2

Alignment Scores:  
Pred. No.: 9,79e-184 Length: 386  
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Best Local Similarity: 93.90% Mismatches: 5  
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US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-10-212-877-2 (1-386)

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Db	221	AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr	240
QY	721	TACTGTGGACTTTATCTCTGAGTCAGAACAGCAAGTGAAGCGAGTGGCTAGTTCTTGAGA	780
Db	241	TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg	260
QY	781	AGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG	840
Db	261	ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal	280
QY	841	TTTCCATATCTCATACAGAAAGTAAAGCAAGACCATGAGCAACTGCTCTAGTAGCC	900
Db	281	PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla	300
QY	901	AGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAATACCAAGGTATACATGGCCAT	960
Db	301	SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHis	320
QY	961	GGCTCAGAACCTTATACCTAGTCTCTGGAGGTGGGACGATTCGATCTATGATTTGGGC	1020
Db	321	GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly	340
QY	1021	ATCAATATTCGTT-----	1034
Db	341	IleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuPro	360
QY	1035	-----TACATCAAAACCCACTCTAGAGAGCTTTTGGCGCTGCTCTAA 1079	
Db	361	GluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLys	377
RESULT 3			
US-10-379-836-17			
; Sequence 17, Application US/10379836			
; Publication No. US20030215850A1			
; GENERAL INFORMATION:			
; APPLICANT: Bristol-Myers Squibb Company			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON			
; TITLE OF INVENTION: TAFI			
; FILE REFERENCE: D0214NP			
; CURRENT APPLICATION NUMBER: US/10/379,836			
; CURRENT FILING DATE: 2003-03-04			
; PRIOR APPLICATION NUMBER: U.S. 60/361,523			
; PRIOR FILING DATE: 2002-03-04			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 17			
; LENGTH: 423			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-379-836-17			
Alignment Scores:			
Pred. No.:	6,71e-182	Length:	423
Score:	1835.00	Matches:	356
Percent Similarity:	86.23%	Conservative:	1
Best Local Similarity:	85.99%	Mismatches:	3
Query Match:	94.98%	Indels:	55

DB:	14	Gaps:	2
US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-379-836-17 (1-423)			
QY	1	ATGAAGCTTTGAGCGCTTGCAGTCCTTGATACCATTTGTTCTCTTCTGTGAGCAGCATGTC	60
Db	1	MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal	20
QY	61	TTCCGGTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA	120
Db	21	PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln	40
QY	121	GTTCTACAGAATCTTACTACAATATGAGATTTGTTCTCTGCGACCGGTAAACAGCTGAC	180
Db	41	ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp	60
QY	181	CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGTCATCTGATGTCACATGTC	240
Db	61	LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal	80
QY	241	AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTCTGTCGACAGCTGGAAGAT	300
Db	81	LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp	100
QY	301	CTTATTCAACAGCAGATTTCCAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTAT	360
Db	101	LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr	120
QY	361	GAACAGTATCACTCAATAATGAAATCTATTTCTTGATAGAATTTATACTGAGGCGAT	420
Db	121	GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis	140
QY	421	CCTGATATGCTTTACAAAATCCACATTTGGATCCTCATTTTGAGAAGTACCACCTCTATGTT	480
Db	141	ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal	160
QY	481	TTAAAGGTTTCTGGAAGAAACAAACAGCAAAATGCCATATGGAATTCAGTGTGAAATC	540
Db	161	LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle	180
QY	541	CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGTTTCTATAGGCCAT-----	591
Db	181	HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln	200
QY	591	-----	591
Db	201	PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet	220
QY	592	-----AATCGAATGTGGAGAAAG	609
Db	221	ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys	240
QY	610	AACCGTTCTTTCTATCGGAACAATCATTCATCGGACAGACCTGATAGCACTTTGTC	669
Db	241	AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla	260
QY	670	TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCGGAAACCTACTGTGA	729
Db	261	SerLysHisTrpCysGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGly	280
QY	730	CTTTATCTCAGTCAGAACCAAGTGAAGCGAGTGGCTAGTTTCTTGAAGAAATATC	789
Db	281	LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle	300
QY	790	AACAGATTAAAGCATACATCAGCATGTCATCTACTCCAGCATATAGTTTCCATAT	849
Db	301	AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr	320
QY	850	TCCTATACAGAAAGTAAAGCAAAAGACCATGAGGAACCTGCTCTCTAGTAGCCAGTGAAGCA	909
Db	321	SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla	340
QY	910	GTTCTGCTATTGACAAATACTAGTAAATAATACCAGGTATACACATGCCCATGCTCAGAA	969

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Db 341 ValArgAlaIleGluLeuThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCATTATACCTAGCTCTCGAGGTGGGACGATTCGATCTATGATTTGGGCATCAAAATAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCCTGTAGAGAGCTTTTCCCTGCTCTCTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 4
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Alignment Scores:
Pred. No.: 9,4e-181 Length: 423
Score: 1824.00 Matches: 354
Percent Similarity: 85.75% Conservative: 1
Best Local Similarity: 85.51% Mismatches: 5
Query Match: 94.41% Indels: 55
DB: Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-813-133A-4 (1-423)
QY 1 ATGAGCTTTTGAGCTTGCAGTCTCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGTTCCAGAGTGGCCAGTTCTAGTGTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
QY 181 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCAATCTGTATGTCGACAAATGTG 240
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTGTGCGAGAGCTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCATTTTCCAAACACACAGTCAGCCCGAGCTCCGCGATCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCAATAAATCTATCTCTGATAGAAATTTATTAAGTGAAGGCAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
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QY 421 CCTGATGCTTACAAAAATCCACATTTGGATTCCTCATTGTGAGAAAGTACCCTACTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTGAAAAGAACAAACAGCCAAAAATGCCATATGCATATGATGACTGTGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
QY 541 CATCCAGAGAAATCGATCTCTCTGCTTTCTGCTTGTGGTTCATAGGCCAT----- 591
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 -----TAC 591
Db 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValAspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
Db 221 ProValValAsnValAspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpArgLys 240
QY 610 AACCGTTCTTTCTATGCGAACCAATCATTTGCATCGGAACAGACCTGAATAGCACTTTGTC 669
Db 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 260
QY 670 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCCTCATGCTCGAAACCTACTGTGGA 729
Db 261 SerLysHisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTGAGTCAGAACACAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAGAAATATC 789
Db 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 300
QY 790 AACGAGATTAAAGCATACATCAGATGTCATTCATCTCCAGCATATAGTGTTCATAT 849
Db 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACACAGCTAAAGCAAGACCATGAGCACTGCTCTAGTAGCCAGCTGAAGCA 909
Db 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAACCTAGTAAAAATACACAGGTATACACATGCGCATGGCTCAGAA 969
Db 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 360
QY 970 ACCTTATACCTAGCTCTCGAGGTGGGACGATTCGATCTATGATTTGGGCATCAAAATAT 1029
Db 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
Db 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCCTGTAGAGAGCTTTTCCCTGCTCTCTAAA 1079
Db 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 5
US-10-212-877-4
; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
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; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Alignment Scores:
Pred. No.: 9,4e-181 Length: 423
Score: 1824.00 Matches: 354
Percent Similarity: 85.75% Conservative: 1
Best Local Similarity: 85.51% Mismatches: 5
Query Match: 94.41% Indels: 55
DB: 14 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-212-877-4 (1-423)

QY 1 ATGAAGCTTTGAGCGCTTCAGCTCCCTGACCATGTTCTCTCTGAGCAGCATGTC 60
DB 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGCTTCAGAGTGGCCAAAGTTCCTAGCTGCTCTCTAGAACCTCTAGGCAAGTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGAATCTTACTACAATAGATTGTTCTCTGCGAGCGCGTAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrThrThrGluIleValLeuTrpGlnProValThrAlaasp 60
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATCTGCACATG 240
DB 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATCAGTGTCTCTGCGCAGACGCTGGAAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaaspValGluasp 100
QY 301 CTTATTCAACAGCAGATTTCCACAGCACAGTCAGCCCGCGCCCTCCGCTACTACT 360
DB 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
QY 361 GAACAGTATCACTCAATAAGAAATCTATTCTTGATAGAAATTTAATCTAGAGGCAT 420
DB 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCATTTGATCTGATCTCTTTCAGAGTACCCACTCTATG 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
QY 481 TTAAGGTTTCTGAAAAAGAACAAACAGCCCAAAATGCCATATGGAATGACTGTGGAATC 540
DB 161 LysLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrpIleaspCysGlyIle 180
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTGTTTCTGTTGTTTCATAGCCAT 591
DB 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGln 200
QY 591 ----- 591
DB 201 PheTyrGlyIleIleGlyGlnTyrThrAsnLeuLeuArgLeuValaspPheTyrValMet 220
QY 592 -----AATCGAATGTGGAGAAAG 609
DB 221 ProValValAsnValaspGlyTyrAspTyrSerTrpLysLysAsnArgMetTrpAglLys 240
QY 610 AACGGTTCTTTCTATGCGAAACAATCAATTCATCGAACAGACTGGAATGCACTTTGTC 669
DB 241 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAla 280
QY 670 TCCMAACACTGGTGTGAGGAGGTGCATCCAGTCTCTCATGCTCGGAAACCTACTGGA 729
DB 261 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 280
QY 730 CTTTATCTCAGTCAGAACCAAGTGAAGCGAGTGGCTAGTTTCTTGAGAGAAATATC 789
DB -----
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DB 281 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 300
QY 790 AACCAGATTAAAGCATACATCAGCATGCATTTCATCATCTCCAGCATATAGTGTTCATAT 849
DB 301 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 320
QY 850 TCCTATACACGAAGTAAAGCAAGACCATCAGGAACCTGTCTCTAGTAGCCAGTGAAGCA 909
DB 321 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 340
QY 910 GTTCGTGCTATTGACAAAACCTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 969
DB 341 ValArgAlaIleGluLysIleSerLysAsnThrArgTyrThrHisGlyHisIleGlySerGlu 360
QY 970 ACCTTATACCTAGCTCCTCGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAAT 1029
DB 361 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 380
QY 1030 TCGTT-----TAC 1037
DB 381 SerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeuLeuProGluArgTyr 400
QY 1038 ATCAAAACCCACTGTAGAGAAAGCTTTTCGCCGCTGTCTCTAAA 1079
DB 401 IleLysProThrCysArgGluAlaPheAlaValSerLys 414

RESULT 6
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Alignment Scores:
Pred. No.: 1,898-179 Length: 428
Score: 1811.50 Matches: 354
Percent Similarity: 84.73% Conservative: 1
Best Local Similarity: 84.49% Mismatches: 5
Query Match: 93.76% Indels: 60
DB: 15 Gaps: 3

US-09-980-881a-1_copy_18_1097 (1-1080) x US-10-115-479-68 (1-428)

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DB 1 MetLysLeuCysSerLeuAlaValLeuValProLleValLeuPheCysGluGlnHisVal 20
QY 61 TTCGGCTTCCAGAGTGGCCAGTCTCTAGTCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
DB 21 PheAlaPheGlnSerGlyGlnValLeuAlaValLeuProArgThrSerArgGlnValGln 40
QY 121 GTTCTACAGATCTTACTACAAATCATGAGATTTGTTCTCTGGCAGCCGGTAACAGCTGAC 180
DB 41 ValLeuGlnAsnLeuThrThrThrTyrrGluLeuValLeuLeuProValThrAlaAsp 60
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTGTAATGTCATCTGATGTCGACAAATGTG 240
DB 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
QY 241 AAAGCCCATTTAAATGTGAGGGGAATTCATGACGATGCTTCTGCTGGCAGAGTGGAGAT 300
DB 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
QY 301 CTTATTCAACAGCAGATTTTCAACGACACAGTACGCCCCCGAGCTCCGCACTCGTACTAT 360
DB 101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrr 120
QY 361 GAACAGTATCACTCACTAAATCAATCTATTCTTGGATAGAAATTTATTAACGTGAGGCGAT 420
DB 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHis 140
QY 421 CCTGATATGCTTACAAAATCCAGATTCGATCCCTCATTTGACAGTACCCACTCTATGTT 480
DB 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrVal 160
QY 481 TTAAG-----GTTTCTCGAAAAGAACAAACAGCCCAAAATGCCATATGG 525
DB 161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTrp 180
QY 526 ATTGACTGTGAATCCATCCAGAGAATGGATCTCTCTGCTTTCTGCTGTGTTGTTGTTATA 585
DB 181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200
QY 586 GGCAT----- 591
DB 201 GlyHisIleThrGlnPheTyrrGlyIleIleGlyGlnTyrrThrAsnLeuLeuArgLeuVal 220
QY 592 -----AAT 594
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DB 221 AspPheTyrrValMetProValValAsnValAspGlyTyrrAspTyrrSerTrpLysAsn 240
QY 595 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTCGCATCGGAACGACTG 654
DB 241 ArgMetTrpArgLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeu 260
QY 655 AATAGCAACTTGTCTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCCTCATGCTCG 714
DB 261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 280
QY 715 GAAACCTACTGTGACATTTTATCTGACTCAGAACCAAGTGAAGGAGTGGCTAGTTTC 774
DB 281 GluThrTyrrCysGlyLeuTyrrProGluSerGluProGluValLysAlaValAlaSerPhe 300
QY 775 TTGAGAAATAATATCAACAGATTAAAGCATATACATCAGCATGCATTCATCTCCAGCAT 834
DB 301 LeuArgArgAsnIleAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHis 320
QY 835 ATAGTGTTCATATTCCTATACAGAAAGTAAAGCAACCACTAGGAACTGCTCTCTA 894
DB 321 IleValPheProTyrrSerTyrrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 340
QY 895 GTAGCCAGTGAAGCAGTTCGTGCTATTGACAAACTAGTAAATAATACAGGTATACACAT 954
DB 341 ValAlaSerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrrThrHis 360
QY 955 GGCATGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGACGATGGATGATATGAT 1014
DB 361 GlyHisGlySerGluThrLeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrrAsp 380
QY 1015 TTGGGCATCAATATTCGTT----- 1034
DB 381 LeuGlyIleLysTyrrSerPheThrIleGluLeuArgAspThrGlyThrTyrrGlyPheLeu 400
QY 1035 -----TACATCAAAACCCACCTGTAGAGAACCTTTTGCCTGCTCTCTATAA 1079
DB 401 LeuProGluArgTyrrIleLysProThrCysArgGluAlaPheAlaValSerLys 419

RESULT 7
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
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Score: 1746.00 Matches: 338  
Percent Similarity: 83.82% Conservative: 9  
Best Local Similarity: 81.64% Mismatches: 13  
Query Match: 90.37% Indels: 55  
DB: 14 Gaps: 2

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-10-379-836-2 (1-423)

QY 1 ATGAAGCTTTGAGCGCTTGCAGCTCTGTACCATTGTTCTCTCTCTGTGAGCAGCATGTC 60  
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
QY 61 TTCGGTTCCAGAGTGGCCAGTCTTACGTCTCTCTCTAGAACCTCTAGCAGTTCAA 120  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 121 GTTCTACAGAATCTTACTACAACTATGAGATTGTTCTCTGCGCAGCCGGTAACAGCTGAC 180  
Db 41 ValLeuGlnAsnLeuThrThrThrTyrrGluIleValLeuTrpGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG 240  
Db 61 LeuIleGluLysLysGlnValHisPhePheValAsnSerSerAspValAspAsnVal 80  
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGCTTCTGCGCAGCTGGAAGAT 300  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTTCACAGACACAGTCAGCCCGAGCTCCGCACTCGTACTAT 360  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrr 120  
QY 361 GAACAGTACTACTAAATGAATATCTTCTGATAGATTAATTAATCACTGAGAGCAT 420  
Db 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluLeuIleThrGluLysTyrr 140  
QY 421 CCTGATATGCTTACAAAATCACATTCGATCCTCATTTGAGAGTACCCACTCTATGTT 480  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerTyrrGluLysHisProLeuTyrrVal 160  
QY 481 TTAAAGGTTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGATTGATCTGGAATC 540  
Db 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaMetTrpIleAspCysGlyIle 180  
QY 541 CATGCCAGAAATGATCT 591  
Db 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisIleThrGlu 200  
QY 591 ----- 591  
Db 201 TyrTyrrGlyIleIleGlyGluTyrrThrAsnLeuLeuArgHisValAspPheTyrrValMet 220  
QY 592 -----AATCGAATGTGGAAGAAG 609  
Db 221 ProValValAsnValAspGlyTyrrAspTyrrSerTrpLysLysAsnArgMetTrpArgLys 240  
QY 610 AACCGTCTTCTATGCGAACAAATCATTCGATCGGAACAGACCTGAAATAGCAACTTTGTC 669  
Db 241 AsnArgSerPheTyrrAlaAsnAsnArgCysIleGlyThrAspLeuAsnArgAsnPheAla 260  
QY 670 TCCAAACACTGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 729  
Db 261 SerLysHisTrpCysGluGluGlyAlaSerPheSerPheSerCysSerGluThrTyrrCysGly 280  
QY 730 CTTTATCTCTGAGTCAAGACCAAGTGAAGGAGGTGAGTCTTCTTCTGAGAAGAAATATC 789  
Db 281 LeuTyrrProGluSerGluProGluAlaLysAlaValAlaAsnPheLeuArgAsnIle 300  
QY 790 AACCAATTAAAGCATATACATAGCATGATTCATTAATCTCCAGCATATAGTGTTCCTATAT 849  
Db 301 AsnHisIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPheProTyrr 320  
QY 850 TCCTATACAGGAAGTAAAGCAAGAACCATGAGGAAGTCTCTCTAGTAGCCAGTGAAGCA 909

Db 321 SerTyrrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 340  
QY 910 GTTCGTGCTATTGACAAAACCTAGTAAAAATACACAGGTATACACATGGCCATGGCTCAGAA 969  
Db 341 ValArgAlaIleGlnLysThrSerLysAsnIleArgTyrrThrHisGlyArgGlySerGlu 360  
QY 970 ACCTTATACCTAGTCTCTGAGGTGGGAGCATTTGGATCTATGATTTGGGCAATCAATAT 1029  
Db 361 ThrLeuTyrrLeuAlaProGlyGlyAlaAspAspTrpIleTyrrAspLeuGlyIleLysTyrr 380  
QY 1030 TCGTT-----TAC 1037  
Db 381 SerPheThrIleGluLeuArgAspThrGlyLysTyrrGlyPheLeuLeuProGluArgTyrr 400  
QY 1038 ATCAAAACCCACCTGTAGAGAGCTTTTCCGCTCTCTCTATAA 1079  
Db 401 IleLysProThrCysLysAspAlaPheAlaValSerLys 414

RESULT 9  
US-10-379-836-18  
; Sequence 18, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; TITLE OF INVENTION: TAFI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-379-836-18

Alignment Scores:  
Pred. No.: 2,97e-152 Length: 422  
Score: 1550.50 Matches: 302  
Percent Similarity: 78.99% Conservative: 25  
Best Local Similarity: 72.95% Mismatches: 32  
Query Match: 80.25% Indels: 56  
DB: 14 Gaps: 3

US-09-980-881A-1\_COPY\_18\_1097 (1-1080) x US-10-379-836-18 (1-422)

QY 1 ATGAAGCTTTGAGCGCTTGCAGCTCTGTACCATTGTTCTCTCTCTGTGAGCAGCATGTC 60  
Db 1 MetLysLeuHisGlyLeuGlyIleLeuValAlaIleIleLeuTyrr---GluGlnHisGly 19  
QY 61 TTCGGTTCCAGAGTGGCCAGTCTAGCTGCTCTCTCTAGAACCTCTAGCAAGTTCAA 120  
Db 20 PheAlaPheGlnSerGlyGlnValLeuSerAlaLeuProArgThrSerArgGlnValGln 39  
QY 121 GTTCTACAGAATCTTACTACAACTATGAGATTGTTCTCTGCGCAGCCGGTAACAGCTGAC 180  
Db 40 LeuLeuGlnAsnLeuThrThrTyrrGluValValLeuTrpGlnProValThrAlaGlu 59  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTG 240  
Db 60 PheIleGluLysLysGluValHisPhePheValAsnAlaSerAspValAspSerVal 79  
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGCTTCTGCGCAGCTGGAAGAT 300  
Db 80 LysAlaHisLeuAsnValSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99  
QY 301 CTTATTCAACAGCAGATTTTCCACGACACAGTACGCCCCGAGCTCCGCACTCGTACTAT 360  
Db 100 LeuIleGluGlnThrPheAsnAspThrValSerProArgAlaSerAlaSerTyrr 119



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QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTGATAGAAATTTATAACTGAGAGCAT 420
Db 120 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluValIleThrGluGlnHis 139
QY 421 CCTGATATGCTTACAAAAATCCCAATTTGGATCTCTCAATTTGAGAAAGTACCCTCTATGTT 480
Db 140 ProAspMetLeuGlnLysIleTyrIleGlySerPheGluLysTyrProLeuTyrVal 159
QY 481 TTAAGGTTCTCGAAAGAAACAAACAGCCAAATGCCAATATGCAATGCACTGTGGAATC 540
Db 160 LeuLysValSerGlyLysGluGlnArgIleLysAsnAlaIleTrpIleAspCysGlyIle 179
QY 541 CATGCCAGAAATGGATCTCTCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 591
Db 180 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyTyrValThrGln 199
QY 591 ----- 591
Db 200 PheHisGlyLysGluAsnLeuTyrThrArgLeuLeuArgHisValAspPheTyrIleMet 219
QY 592 -----AATCGAATGTGGGAAG 609
Db 220 ProValMetAsnValAspGlyTyrAspTyrThrTrpLysLysAsnArgMetTrpArgLys 239
QY 610 AACCGTTCTTCTATCGCAACAAATCATTCGACGACAGACCTGAATAGCAACTTTGTC 669
Db 240 AsnArgSerAlaHisLysAsnAsnArgCysValGlyThrAspLeuAsnArgAsnPheAla 259
QY 670 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGA 729
Db 260 SerLysHisTrpCysGluLysGlyAlaSerSerSerCysSerGluThrTyrCysGly 279
QY 730 CTTTATCTCGAGTCAGAACAGAACAGAGTGAAGGAGTGGCTAGTTCTTGTGAAGAAATATC 789
Db 280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgArgAsnIle 299
QY 790 AACCAATTAACATACATCACATGCATTCATCTACTCCAGCATATAGTTTCCATAT 849
Db 300 AspHisLysAlaTyrIleSerMetHisSerTyrSerGlnGlnLeuLeuPheProTyr 319
QY 850 TCCTATACAGAAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCAGTGAAGCA 909
Db 320 SerTyrAsnArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 339
QY 910 GTTCGTGCTATTGACAAAACACTAGTAAATACAGGTATACATGCGCATGCTCAGAA 969
Db 340 ValArgAlaIleGluSerLysAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359
QY 970 ACCTTATACCTAGTCTCTGAGTGGGACGATGGATGATCTATGATTTGGGCATCAATAT 1029
Db 360 SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleTyr 379
QY 1030 TCGTT -----TAC 1037
Db 380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgTyr 399
QY 1038 ATCAAAACCCACTGTAGAGAGCTTTTGGCGCTGTCTCTAAA 1079
Db 400 IleLysProThrCysAlaGluAlaLeuAlaAlaIleSerLys 413

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RESULT 10

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US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523

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; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.12
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Alignment Scores:
Pred. No.: 2,46e-149 Length: 422
Score: 1522.50 Matches: 297
Percent Similarity: 78.02% Conservative: 26
Best Local Similarity: 71.74% Mismatches: 36
Query Match: 78.80% Indels: 56
DB: 14 Gaps: 3

US-09-980-881a-1_COPY_18_1097 (1-1080) x US-10-379-836-16 (1-422)

QY 1 ATGAAGCTTTGCGAGCTTGCAGCTTGCAGCTTGTACCATCTTCTTGTGAGCAGCATGTC 60
Db 1 MetLysLeuTyrGlyLeuValValAlaIleLeuTyr---GluLysHisGly 19
QY 61 TTCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 20 LeuAlaPheGlnSerGlyHisValLeuSerAlaLeuProArgThrSerArgGlnValGln 39
QY 121 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGCGCCGCTACAGCTGAC 180
Db 40 LeuLeuGlnAsnLeuThrThrTyrGluValValLeuTrpGlnProValThrAlaGlu 59
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATCTCCACAATGTG 240
Db 60 PheIleGluLysLysLysGluValHisPhePheValAsnAlaSerAspValAsnSerVal 79
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGACGTGCTTCTGCTGCGACGCTGGAAGAT 300
Db 80 LysAlaTyrLeuAsnAlaSerArgIleProPheAsnValLeuMetAsnAsnValGluAsp 99
QY 301 CTTATTCACAGCAGATTTCCACGACAGTCAGTCCAGCCCGCCGCTCCGCTACTACTAT 360
Db 100 LeuIleGlnGlnThrSerAsnAspThrValSerProArgAlaSerSerSerTyrTyr 119
QY 361 GAACAGTATCACTCACTAAATCAAATCTATTCTTGATAGAATTTATTAATCAGAGGCAT 420
Db 120 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluValIleThrGluGlnHis 139
QY 421 CCTGATATGCTTACAAAAATCCCAATTTGGATCTCTCAATTTGAGAAAGTACCCTCTATGTT 480
Db 140 ProAspMetLeuGlnLysIleTyrIleGlySerSerTyrGluLysTyrProLeuTyrVal 159
QY 481 TTAAGGTTCTCGAAAGAAACAAACAGCCAAATGCCAATATGCAATGCACTGTGGAATC 540
Db 160 LeuLysValSerGlyLysGluHisArgValLysAsnAlaIleTrpIleAspCysGlyIle 179
QY 541 CATGCCAGAAATGGATCTCTCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 591
Db 180 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyTyrValThrGln 199
QY 591 ----- 591
Db 200 PheHisGlyLysGluAsnThrTyrThrArgLeuLeuArgHisValAspPheTyrIleMet 219
QY 592 -----AATCGAATGTGGGAAG 609
Db 220 ProValMetAsnValAspGlyTyrAspTyrThrTrpLysLysAsnArgMetTrpArgLys 239
QY 610 AACCGTTCTTCTATCGCAACAAATCATTCGACGACAGACCTGAATAGCAACTTTGTC 669
Db 240 AsnArgSerValHisMetAsnAsnArgCysValGlyThrAspLeuAsnArgAsnPheAla 259
QY 670 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGA 729

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Db 260 SerLysHisTrpCysGluLysGlyAlaSerSerPheSerCysSerGluThrTyrCysGly 279
Qy 730 CTTTATCTGAGTCAGAACCAAGTGAAGCAGTGGCTAGTTCTTTCGAGAAGAAATATC 789
Db 280 LeuTyrProGluSerGluProGluValLysAlaValAlaAspPheLeuArgAsnile 299
Qy 790 AACAGATTAAGCATACATCGCATGCTATCTACTCCAGCATATAGTGTTCATAT 849
Db 300 AsnHisIleLysAlaTyrIleSerMetHisSerTyrSerGlnGlnIleLeuPheProTyr 319
Qy 850 TCCTATACAGCAAGTAAAGCAACACACATGAGGAACTGCTCTAGTAGCCAGTGAAGCA 909
Db 320 SerTyrAsnArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 339
Qy 910 GTTCGTGCTATTGACAAAACCTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 969
Db 340 ValArgAlaIleGluSerIleAsnLysAsnThrArgTyrThrHisGlySerGlySerGlu 359
Qy 970 ACCTTATACCTAGCTCCTGGAGGTGGGACGATGGCATCTATGATTTGGGCATCAATAT 1029
Db 360 SerLeuTyrLeuAlaProGlyGlySerAspAspTrpIleTyrAspLeuGlyIleLysTyr 379
Qy 1030 TCGTTTACATC----- 1040
Db 380 SerPheThrIleGluLeuArgAspThrGlyArgTyrGlyPheLeuLeuProGluArgPhe 399
Qy 1041 ---AAACCCACCTGTAGAGAGCTTTTCCCGCTGTCTCTAAA 1079
Db 400 IleLysProThrCysAlaGluAlaLeuAlaValSerLys 413

RESULT 11
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
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; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Alignment Scores:
Pred. No.: 4.9e-141 Length: 322
Score: 1442.50 Matches: 292
Percent Similarity: 77.72% Conservative: 1
Best Local Similarity: 77.45% Mismatches: 3
Query Match: 74.66% Indels: 82
DB: 15 Gaps: 2

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-10-115-479-64 (1-322)

Qy 1 ATGAAGCTTTGCACGCTTGCAGTCCTTGTACCCATGTTCTCTCTGTGACGACATGTC 60
Db 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Qy 61 TTGCGGTTCCAGAGTGGCCAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Qy 121 GTTCTACAGATCTTACTACAAATATGAGATTGTTCTTGGCAGCCGGTAAACAGTGC 180
Db 41 ValLeuGlnAsnLeuThrThrTyrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Qy 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTCTTAATGTCATCTGTGTCGACAACTGTG 240
Db 61 LeuIleValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Qy 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTCTTGTGGCAGACGTGGAAGAT 300
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Qy 301 CTTATTCAACAGCAGATTTCCACGACACAGTACGCCCCCGAGCTCCGCACTCGTACTAT 360
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Qy 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGTAGAATTTATTAACCTGAGGCGAT 420
Db 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Qy 421 CCTGATATGCTTACAAAAATCCACATTGGATTCCTCATTTGAGAAAGTACCCACTCTATGTT 480
Db 141 ProAspMetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrVal 160
Qy 481 TTAAGGTTTCTGAAAGAAACAAACACGCCAAAATATGTCATATGATGATCTGTGGAATC 540
Db 161 LeuLysValSerGlyLysGluGlnAlaAlaLysAsnAlaIleTyrPileAsp----- 177
Qy 541 CATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTGTGGTTCATAGGCCAATAATCGAATG 600
Db 177 ----- 177
Qy 601 TGGAGAAAGAACCGTTCTTTCTATCGGAACAATCATTTGTCATCGGAACAGACCTGTAATAGC 660
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Db 177 ----- 177  
QY 661 AACTTTGCTCCAAACACTGGTGTGAGGAAGTGATCCAGTTCCTCATGCTCGGAACCC 720  
Db 177 ----- 177  
QY 721 TACTGTGGACTTTATCTCAGTCAGAACAGGAGGAGGAGTGGCTAGTTTCTTTGAGA 780  
Db 178 ---CysGlyLeuTyrrProGluSerGluProGluValAlaValAlaSerPheLeuArg 196  
QY 781 AGAAATATCAACAGATTAAGCATACATCAGCATGCTATCATCTCCAGCATATAGTG 840  
Db 197 ArgAsnIleAsnGlnIleLysAlaTyrlleSerMetHisSerTy-SerGlnHisIleVal 216  
QY 841 TTTCATATCTATACAGAGTAAGCAAGCAAGACCATCAGGAACTGCTCTAGTAGCC 900  
Db 217 PheProTy-SerTyrrThrArgSerLysSerLysAspHisGluLysSerLeuValAla 236  
QY 901 AGTGAAGCAGTTCCTCTATTGACAAACTAGTAAAAATACCAAGGTATACATGCCCAT 960  
Db 237 SerGluAlaValArgAlaIleGluLysIleSerLysAsnThrArgTyrrHisGlyHis 256  
QY 961 GGCCTAGAACCTTATACCTAGCTCTCGAGGTGGGAGCATGGATCTATGATTTGGGC 1020  
Db 257 GlySerGluThrLeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrrAspLeuGly 276  
QY 1021 ATCAATATTCGTT----- 1034  
Db 277 IleLysTy-SerPheThrIleGluLeuArgAspThrGlyThrTyrrGlyPheLeuLeuPro 296  
QY 1035 -----TACATCAAAACCCACTCTAGAGAGCTTTTGGCGCTGCTCTCTAA 1079  
Db 297 GluArgTyrrIleLysProThrCysArgGluAlaPheAlaValSerLys 313

RESULT 12  
US-10-115-479-66  
; Sequence 66. Application US/10115479  
; Publication NO. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zernhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 66  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-66  
Alignment Scores:  
Pred. No.: 3,14e-136 Length: 354  
Score: 1396.50 Matches: 282  
Percent Similarity: 67.30% Conservative: 0  
Best Local Similarity: 67.30% Mismatches: 4  
Query Match: 72.28% Indels: 134  
DB: 15 Gaps: 4  
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QY 61 TTCGGTTCACAGTGGCCAGTCTTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
Db 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
QY 121 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 180  
Db 41 ValLeuGlnAsnLeuThrThrTyrrGluIleValLeuTyrGlnProValThrAlaAsp 60  
QY 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTTGTAAATGCATCTGATCTCGACAATGTC 240  
Db 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80  
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATTCAGTGTCTTGTGGCAGACGTGGAAGAT 300  
Db 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
QY 301 CTTATTCAACAGCAGATTTTCCAAACGACACAGCAGCCCGCCGCTCCGATCTGCTACTAT 360  
Db 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrr 120  
QY 361 GAACAGTATCCTCACTAAATGAAATCTATTCTTGATAGAAATTTTAACTGAGAGGCAT 420  
Db 121 GluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGluPheIleThrGluArgHis 140  
QY 421 CCTGATATGCTTACAAAAATCCACATTGGATCTCTATTGAGAGTACCACCTCTATGTT 480  
Db 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrVal 160  
QY 481 TTAAG-----GTTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGG 525  
Db 161 LeuLysGlyPhePheGluGlnValSerGlyLysGluGlnAlaLysAsnAlaIleTrp 180  
QY 526 ATTGACTGTGGAATCCATCCAGAGAAATGATCTCTCTGCTTTCTGCTTGTGTTTCATA 585

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Db 181 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 200
Qy 586 GCCCAT----- 591
Db 201 GlyHisIleThrGlnPheTyrGlyIleIleGlyGlnTyrThrAsnLeuArgLeuVal 220
Qy 592 -----AAT 594
Db 221 AspPheTyrValMetProValValAsnValAspGlyTyrAspTyrSerTrpIleValAsn 240
Qy 595 CGAATGTGGAGAAAGACCGTTCTTCTATGCGAACAATCATGTCATCGGAACACACCTG 654
Db 241 ArgMetTrpArgAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 260
Qy 655 AATGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCG 714
Db 261 AsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 280
Qy 715 GAAACCTACTGTGGACTTTATCTCAGTCAGACAGAACAGAGTGAAGGCAGTGGCTAGTTTC 774
Db 281 GluThrTyrCysGlyLeuTyrProGlu----- 289
Qy 775 TTGAGAAGAAATATCAACAGATTAAAGCATACATACAGATGCATTATCATCTCCAGCAT 834
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Qy 835 ATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGCAATGAGGAACTGTCTCTA 894
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Qy 895 GTAGCCAGTGAAGCAGTTCGTCTATTGACAAACTAGTAAATAACACAGGTATACAT 954
Db 289 ----- 289
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Db 290 -----SerGluThrLeuTyrLeuAlaProGlyGlyAspTrpIleTyrAsp 306
Qy 1015 TTGGCATCAATATTCGTT----- 1034
Db 307 LeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrTyrGlyPheLeu 326
Qy 1035 -----TACATCAAAACCCCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1079
Db 327 LeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSerLys 345

RESULT 13
US-09-925-302-467
; Sequence 467, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.: 3,326-78 Length: 211
Score: 839.00 Matches: 164
Percent Similarity: 82.59% Conservative: 2
Best Local Similarity: 81.59% Mismatches: 9

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Query Match: 43.43% Indels: 27
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Db 3 TrpIleSer---MetLeuCysArgTrpLeuMetTrpMetValMetAsnTyrSerTrpLys 21
Qy 589 CATAATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACAATCATGTCATCGGAACA 648
Db 22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThr 41
Qy 649 GACTGTAATACCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCA 708
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Qy 709 TGCTCGGAAACCTACTGTGACTTTATCCTGAGTCAGAACCCAGAGTGAAGGCAGTGGCT 768
Db 62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAla 81
Qy 769 AGTTCTTCTGAGAAATATCAACAGATTAAAGCATACATCAGCATGTCATCTACTCTCC 828
Db 82 SerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSer 101
Qy 829 CAGATATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGCAATGAGGAACCTG 888
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Qy 949 ACACATGCCATGCTCAGAAACCTTATACCTAGCTCTCTGAGTGGGAGCAGATTGGATC 1008
Db 142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161
Qy 1009 TATGATTGGGCATCAATATTCGTT----- 1034
Db 162 TyrAspLeuGlyIleLysTyrSerPheThrIleGluLeuArgAspThrGlyThrGly 181
Qy 1035 -----TACATCAAAACCCCTGTAGAGAAGCTTTTGGCGCTGTCTCT 1076
Db 182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSer 201
Qy 1077 AAA 1079
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RESULT 14
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Alignment Scores:
Pred. No.: 3,326-78 Length: 211

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Score: 839.00 Matches: 164
Percent Similarity: 82.5% Conservativity: 2
Best Local Similarity: 81.5% Mismatches: 9
Query Match: 43.4% Indels: 27
DB: 10 Gaps: 3

US-09-980-881A-1_COPY_18_1097 (1-1080) x US-09-925-302-467 (1-211)
QY 553 TCGATCTCTCGCTTCTGCTTGGTTCATA-----GGC 588
Db 3 TrpIleSer--MetLeuCysArgTrpLeuMetTrpMetValMetAsnTyrSerTrpLys 21
QY 589 CATAATCGAATGTGAGAAAGACGCTTCTTCTATGCGAACAAATCATTTGCATCGGAACA 648
Db 22 LysAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThr 41
QY 649 GACCTGAATAGCAATTTCTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCA 708
Db 42 AspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSer 61
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Db 62 CysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAla 81
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QY 829 CAGCATATAGTGTTCATATTCCTATACACGAAGTAAAGCAAGACCATCAGGAATG 888
Db 102 GlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeu 121
QY 889 TCTTAGTACGACGAGTGTCTGCTGCTATTGACAAATAGTAAATAATACCATGAT 948
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Db 142 ThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIle 161
QY 1009 TATGATTGGGCATCAATATTCGTT----- 1034
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QY 1035 -----TACATCAAAACCCACTGTAGAGAGCTTTTCCCGCTGCTCT 1076
Db 182 PheLeuLeuProGluArgTyrIleLysProThrCysArgGluAlaPheAlaValSer 201
QY 1077 AAA 1079
Db 202 Lys 202

RESULT 15
US-10-074-978A-269
; Sequence 269, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
```

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; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074, 978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268, 221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335, 109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312, 284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268, 496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276, 703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330, 293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322, 127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280, 899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310, 797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268, 646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-074-978A-269

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Query Match: 33.44% Indels: 44
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Db 21 HisPheGluGlyGluLysValPheArgValAsnValGluAspGluAsnAspIleSerLeu 40
QY 124 CTACAGAATCTTACTACACATATGAGATTGTTCTTGGCAGCCGCTAACAGCTGACCTT 183
Db 41 LeuHisGluLeuAlaSerThrArgGlnIleAspPheTrpLysProAspSerValThrGln 60
QY 184 ATTGTGAAGAAAAAACAAGTCCATCTTTTGTAAATGTCATGTCGACAAATGTGAAA 243
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Qy 364 CAGTATCACTCACTAAATCAATCTTCTTGGATAGAAATTTATAACTGAGAGGCATCCT 423
Db 118 LysTyrAsnAsnTrpGluThrIleGluAlaTrpThrLysGlnValThrSerGluAsnPro 137
Qy 424 GATATGCTTACMAAATCCATCGATCCCTCAATTTGAGAAGTACCCACTCTATGTTTAA 483
Db 138 AspLeuIleSerArgThrAlaIleGlyThrPheLeuGlyAsnAsnIleTyrLeuLeu 157
Qy 484 AAGGTTTCTGGAAGAACAAACAGCCAAATAATGCCATATGATTTGACTGTGGAATCCAT 543
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Qy 586 -----GGCCAT-----AATCGAATGTGGAGAAAGAAC 612
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Qy 613 CGTCTTCTATCGAACAATCAATTCGACGACAGACCTCAATAGCAACTTTGTCTCC 672
Db 237 ArgSerThrAsnAlaGlyThrThrCysIleGlyThrAspProAsnArgAsnPhe---Asp 255
Qy 673 AAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTT 732
Db 256 AlaGlyTrpCysThrThrGlyAlaSerThrAspProCysAspGluThrTyrCysGlySer 275
Qy 733 TATCTGTAGTCAGACCAAGTGAAGCAGTGGCTAGTTCTTCTGAGAGAAATATCAAC 792
Db 276 AlaAlaGluSerGluLysGluThrLysAlaLeuAlaAspPheIleArgAsnAsnLeuSer 295
Qy 793 CAGATTAAAGCATACATCAGCATTCATCTCCAGCATATAGTGTTCCTATATTC 852
Db 296 SerIleLysAlaTyrLeuThrIleHisSerTyrSerGlnMetIleLeuTyrProTyrSer 315
Qy 853 TATACAGGAAGTAAAGCAAGACCATGAGGAACTGTCTCTAGTAGCCAGTGAAGCAGTT 912
Db 316 TyrAspTyrLysLeuProGluAsnAsnAlaGluLeuAsnAsnLeuAlaLysAlaVal 335
Qy 913 CGTGTATTGACAAACTAGTAAATAATACCAGGTATACACATGGCGATGGCTCAGAAACC 972
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
6397.100 Million cell updates/sec

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Perfect score: 1080  
Sequence: 1 atgaagctttgcagcttgc.....ttttgcccgtgtctcttaaaa 1080

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	909	84.2	1272	2	US-08-869-057-1
3	909	84.2	1749	1	US-07-649-591B-2
4	909	84.2	1749	1	US-08-277-540-2
5	909	84.2	1749	1	US-08-430-787A-2
6	204	18.9	55827	4	US-09-813-133A-3
7	124	11.5	927	2	US-08-782-760-5
8	124	11.5	927	5	PCT-US96-00995-5
9	123.4	11.4	921	1	US-08-696-139-3
10	123.4	11.4	1215	1	US-08-696-139-1
11	109	10.1	1263	4	US-09-011-769A-38
12	107.6	10.0	1622	4	US-09-023-655-1020
13	107.4	9.9	999	2	US-08-860-882A-67
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15	107.4	9.9	1053	2	US-08-860-882A-64
16	107.4	9.9	1053	4	US-09-011-769A-46
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18	107.4	9.9	1284	2	US-08-860-882A-71
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25	104.2	9.6	1059	4	US-09-011-769A-63
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27	101	9.4	2154	3	US-09-171-945-124

28	92.8	8.6	1311	4	US-09-675-305-9	Sequence 9, Appli
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38	83.6	7.7	945	4	US-10-200-910-3	Sequence 3, Appli
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43	71.6	6.6	1251	3	US-08-640-906-3	Sequence 3, Appli
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45	70.6	6.5	1251	3	US-08-640-906-1	Sequence 1, Appli

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Query Match 94.9%; Score 1025.2; DB 4; Length 1625;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	ATGAAGCTTTG	CAGCCTTGC	AGTCCCTG	TGACCATTTG	TTCTTCTG	TGAGCAGCATGTC	60
Db	17	ATGAAGCTTTG	CAGCCTTGC	AGTCCCTG	TGACCATTTG	TTCTTCTG	TGAGCAGCATGTC	76
QY	61	TTTCGGTTCC	AGTGGCCAA	GTCTTAG	CTCTTCTAG	AACCTCT	TAGGCAAGTTCAA	120
Db	77	TTTCGGTTCC	AGTGGCCAA	GTCTTAG	CTCTTCTAG	AACCTCT	TAGGCAAGTTCAA	136
QY	121	GTCTTACAGA	ATCTTACT	ACAACAT	ATAGATTTG	TTCTCTG	GCGCGGTAA	180
Db	137	GTCTTACAGA	ATCTTACT	ACAACAT	ATAGATTTG	TTCTCTG	GCGCGGTAA	196
QY	181	CTTATTGTGA	AGAAAAA	CAAGTCC	ATTTTGT	TGTAATG	CAATGTCGCAATGTG	240
Db	197	CTTATTGTGA	AGAAAAA	CAAGTCC	ATTTTGT	TGTAATG	CAATGTCGCAATGTG	256
QY	241	AAAGCCCAT	TAAATG	TGAGCGGA	ATTTCC	ATGAGT	CTTGTGCGACAGTGGAGAT	300
Db	257	AAAGCCCAT	TAAATG	TGAGCGGA	ATTTCC	ATGAGT	CTTGTGCGAGATGTTGAGAT	316
QY	301	CTTATTCA	CAGCAGAT	TTTCCA	ACGACAC	AGTCA	GCGCCCGGAGCTCCG	360
Db	317	CTTATTCA	CAGCAGAT	TTTCCA	ACGACAC	AGTCA	GCGCCCGGAGCTCCG	376
QY	361	GAA	CAGTAT	CATCT	CACTAA	ATGAAAT	TTTATTTGATAGAAATTT	420

ALIGNMENTS







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Db 641 TTCTATGGGATATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700
Qy 592 -----AATCGAATGTGGAGAAAG 609
Db 701 CCGGTGGTTAATGTGCGGTTATGACTACTCATGCGAAAGAAATCGAATGTGGAGAAAG 760
Qy 610 AACCGTTCTTTCTATGCGAACAATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGTC 669
Db 761 AACCGTTCTTTCTATGCGAACAATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGCT 820
Qy 670 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 729
Db 821 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 880
Qy 730 CTTTATCCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTGTCTTCTGAGAGAAATATC 789
Db 881 CTTTATCCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTGTCTTCTGAGAGAAATATC 940
Qy 790 AACAGATTAAGCATATACATCAGCATGATTCATCTACTCCAGCATATAGTGTTCATAT 849
Db 941 AACAGATTAAGCATATACATCAGCATGATTCATCTACTCCAGCATATAGTGTTCATAT 1000
Qy 850 TCCTATACAGAGTAAAGCAAGCAAGCAACCATGAGGAACTGTCTTAGTAGCCAGTGAAGCA 909
Db 1001 TCCTATACAGAGTAAAGCAAGCAAGCAACCATGAGGAACTGTCTTAGTAGCCAGTGAAGCA 1060
Qy 910 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 969
Db 1061 GTTCGTGCTATTGACAAAACTAGTAAAAATACCAGGTATACACATGGCCATGGCTCAGAA 1120
Qy 970 ACCTTATACCTAGTCTCTGGAGGTGGGAGCGATTCGATCTATGATTTGGGCATCAAAAT 1029
Db 1121 ACCTTATACCTAGTCTCTGGAGGTGGGAGCGATTCGATCTATGATTTGGGCATCAAAAT 1180
Qy 1030 TCGTTTACA 1038
Db 1181 TCGTTTACA 1189

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RESULT 4

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US-08-277-540-2 Application US/08277540
; Sequence 2, Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Hasak, Janet E. 28,616
; REGISTRATION NUMBER: 689D1C1D1
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Query Match 84.2%; Score 909; DB 1; Length 1749;
Best Local Similarity 89.9%; Pred. No. 7.2e-281;
Matches 1033; Conservative 0; Mismatches 5; Indels 111; Gaps 1;

Qy 1 ATGAAGCTTTTCAGCGCTTGCAGTCTTGTACCCCAATGTTCTTCTGTGAGCAGCATGTC 60
Db 41 ATGAAGCTTTTCAGCGCTTGCAGTCTTGTACCCCAATGTTCTTCTGTGAGCAGCATGTC 100
Qy 61 TTCCGGTTTCCAGAGTGGCCAAAGTTCTAGTCTCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
Db 101 TTCCGGTTTCCAGAGTGGCCAAAGTTCTAGTCTCTCTTCTAGAACCTCTAGGCAAGTTCAA 160
Qy 121 GTTCTACAGAACTTTACTTACAAATATAGAGATTGTTCTCTGGCAGCCGGTAAACAGTCA 180
Db 161 GTTCTACAGAACTTTACTTACAAATATAGAGATTGTTCTCTGGCAGCCGGTAAACAGTCA 220
Qy 181 CTTATTGGAAGAAAAAACAAGTCCATTTTGTAAATGCAATCTGATGTGCAAAATGTG 240
Db 221 CTTATTGGAAGAAAAAACAAGTCCATTTTGTAAATGCAATCTGATGTGCAAAATGTG 280
Qy 241 AAAGCCCAATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGTGGCAGAGCTGGAAGAT 300
Db 281 AAAGCCCAATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGTGGCAGAGCTGGAAGAT 340
Qy 301 CTTATTCAACAGCAGATTTTCCAAACAGACACAGTACGCCCCCGAGCTCCGCAATCGTACT 360
Db 341 CTTATTCAACAGCAGATTTTCCAAACAGACACAGTACGCCCCCGAGCTCCGCAATCGTACT 400
Qy 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGAT 420
Db 401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGAT 460
Qy 421 CTTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAAGTACCCACTCTATGTT 480
Db 461 CTTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAAGTACCCACTCTATGTT 520
Qy 481 TTAAGAGTTTCTGGAAAGAAACAAACAGCCAAAAATGCAATATGGAATGATCTGTGGAATC 540
Db 521 TTAAGAGTTTCTGGAAAGAAACAAACAGCCAAAAATGCAATATGGAATGATCTGTGGAATC 580
Qy 541 CATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 591
Db 581 CATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 640
Qy 592 -----AATCGAATGTGGAGAAAG 609
Db 701 CCGGTGGTTAATGTGCGGTTATGACTACTCATGCGAAAGAAATCGAATGTGGAGAAAG 760
Qy 610 AACCGTTCTTTCTATGCGAACAATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGTC 669
Db 761 AACCGTTCTTTCTATGCGAACAATCATTTGCGATCGGAACAGACCTGAAATAGCACTTTGCT 820
Qy 670 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 729

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Db 821 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGA 880  
Qy 730 CTTTATCCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTCTTCTTGAGAAAGAAATATC 789  
Db 881 CTTTATCCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTCTTCTTGAGAAAGAAATATC 940  
Qy 790 ACCAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 849  
Db 941 ACCAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 1000  
Qy 850 TCCATACAGAAAGTAAAGCAAGCAACCAAGCAATGAGCACTGTCTAGTAGCCAGTGAAGCA 909  
Db 1001 TCCATACAGAAAGTAAAGCAAGCAAGCAATGAGCACTGTCTAGTAGCCAGTGAAGCA 1060  
Qy 910 GTTGGTGTATTGACAAAACCTAGTAAATAACAGGTATACACATGGCCCATGGCTCAGAA 969  
Db 1061 GTTGGTGTATTGACAAAACCTAGTAAATAACAGGTATACACATGGCCCATGGCTCAGAA 1120  
Qy 970 ACCTTATACCTAGTCTCTGAGTGGGAGCATTTGGATCTATGATTTGGGCATCAAATAT 1029  
Db 1121 ACCTTATACCTAGTCTCTGAGTGGGAGCATTTGGATCTATGATTTGGGCATCAAATAT 1180  
Qy 1030 TCGTTTACA 1038  
Db 1181 TCGTTTACA 1189

RESULT 5

US-08-430-787A-2  
; Sequence 2, Application US/08430787A  
; Patent No. 553674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 553674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-430-787A-2  
Query Match 84.2%; Score 909; DB 1; Length 1749;  
Best Local Similarity 89.9%; Pred. No. 7.2e-281;  
Matches 1033; Conservative 0; Mismatches 5; Indels 111; Gaps 1;  
Qy 1 ATGAAGCTTTGCAGCTTGCAGTCTCTACCCATTGTTCTCTCTGTGAGCAGCATGTC 60  
Db 41 ATGAAGCTTTGCAGCTTGCAGTCTCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 100  
Qy 61 TTCCGGTTTCCAGAGTGGCCAAAGTCTTAGTCTGCTTCTCTAGAACCTCTAGGCAAGTTCAA 120  
Db 101 TTCCGGTTTCCAGAGTGGCCAAAGTCTTAGTCTGCTTCTCTAGAACCTCTAGGCAAGTTCAA 160  
Qy 121 GTTCTACAGAAATCTTATCAACAATATAGAGATTGTTCTCTGCGAGCGGTAAACAGCTGAC 180  
Db 161 GTTCTACAGAAATCTTATCAACAATATAGAGATTGTTCTCTGCGAGCGGTAAACAGCTGAC 220  
Qy 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGTCATCTGATGTCGACAAATGTG 240  
Db 221 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGTCATCTGATGTCGACAAATGTG 280  
Qy 241 AAAGGCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGCGAGACGCTGGAAGAT 300  
Db 281 AAAGGCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGCGAGACGCTGGAAGAT 340  
Qy 301 CTTATTCAACAGCAGATTTCACACACAGCAGTCCGAGCCCGAGCCCTCCGATCGTACTAT 360  
Db 341 CTTATTCAACAGCAGATTTCACACACAGCAGTCCGAGCCCGAGCCCTCCGATCGTACTAT 400  
Qy 361 GAACAGTATCACTCAATAAATCAAAATCTATCTCGATAGAAATTTATTAATCTGAGAGCAT 420  
Db 401 GAACAGTATCACTCAATAAATCAAAATCTATCTCGATAGAAATTTATTAATCTGAGAGCAT 460  
Qy 421 CCGTATATGCTTACAAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCACCTCTATGTT 480  
Db 461 CCGTATATGCTTACAAAAATCCACATTTGGATCCTCATTTTGAGAAAGTACCACCTCTATGTT 520  
Qy 481 TTAAAGTTTCTGGAAAGAAACAAACAGCAGCAAAATGCCATATGGAATTCAGTGTGGAATC 540  
Db 521 TTAAAGTTTCTGGAAAGAAACAAACAGCAGCAAAATGCCATATGGAATTCAGTGTGGAATC 580  
Qy 541 CATGCCAGAAATGGAATCTCTCTCTGTTTCTGCTGTGCTTCTATAGCCCAT----- 591  
Db 581 CATGCCAGAAATGGAATCTCTCTCTGTTTCTGCTGTGCTTCTATAGCCCATATAACTCAA 640  
Qy 592 ----- 591  
Db 641 TTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATG 700  
Qy 592 -----AATCGAATGTGGAGAAAG 609  
Db 701 CCGGTGTTTAAATGTGGACGGTTATGACTACTCATGGAAAAAGAAATCGAATGTGGAGAAAG 760  
Qy 610 AACCGTTCTTCTATCGGAACATCATTCATCGGACAGACCTGGAATAGCACTTTGTC 669  
Db 761 AACCGTTCTTCTATCGGAACATCATTCATCGGACAGACCTGGAATAGCACTTTGTC 820  
Qy 670 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAAACTACTGTGGA 729  
Db 821 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAAACTACTGTGGA 880  
Qy 730 CTTTATCCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTGTCTTTGAGAAAGAAATATC 789  
Db 881 CTTTATCCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTGTCTTTGAGAAAGAAATATC 940  
Qy 790 AACCAAGTTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 849  
Db 941 AACCAAGTTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATAT 1000

QY 850 TCCTATACAGAGTAAAGCAAGACCATGAGGAAGTCTCTAGTAGCCAGTGAAGCA 909  
Db 1001 TCCTATACAGAGTAAAGCAAGACCATGAGGAAGTCTCTAGTAGCCAGTGAAGCA 1060  
QY 910 GTTCGTGCTATTGACAAACTAGTAAATAACACAGGTATACACATGGCCATGGCTCAGAA 969  
Db 1061 GTTCGTGCTATTGACAAACTAGTAAATAACACAGGTATACACATGGCCATGGCTCAGAA 1120  
QY 970 ACCTTATACCTAGCTCCTGGAGTGGGACGATTCGATCTATGATTTGGGCATCAAAATAT 1029  
Db 1121 ACCTTATACCTAGCTCCTGGAGTGGGACGATTCGATCTATGATTTGGGCATCAAAATAT 1180  
QY 1030 TCGTTTACA 1038  
Db 1181 TCGTTTACA 1189

RESULT 6  
US-09-813-133A-3  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3

Query Match 18.9%; Score 204; DB 4; Length 55827;  
Best Local Similarity 100.0%; Pred. No. 5.6e-54;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 685 GAGGAGGTGATCCAGTTCCTCATGCTCGGAAACCTACTGGAAGTCTTATCTGAGTCA 744  
Db 48643 GAGGAGGTGATCCAGTTCCTCATGCTCGGAAACCTACTGGAAGTCTTATCTGAGTCA 48702  
QY 745 GAACAGAGTGAAGGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 804  
Db 48703 GAACAGAGTGAAGGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 48762  
QY 805 TACATCAGATGATTCATCTACCTCCAGCATATAGTGTTCATATTCCTATACAGAAAT 864  
Db 48763 TACATCAGATGATTCATCTACCTCCAGCATATAGTGTTCATATTCCTATACAGAAAT 48822  
QY 865 AAACAGAAAGACCATGAGAACTG 888  
Db 48823 AAACAGAAAGACCATGAGAACTG 48846

RESULT 7  
US-08-782-760-5  
; Sequence 5, Application US/08782760  
; Patent No. 5948688  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Jacob  
; APPLICANT: Fulga, Netta  
; APPLICANT: Mendelovitch, Simona  
; APPLICANT: Gorecki, Marian  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/782,760  
FILING DATE: 13-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/378,233  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0336/43847  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 927 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..927  
US-08-782-760-5

Query Match 11.5%; Score 124; DB 2; Length 927;  
Best Local Similarity 57.9%; Pred. No. 2.1e-29;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;  
QY 596 GAATGTGAGAAAGAACCGTTCTTTCTATGGAACAATCATTTGATCGAAGACGACCTGA 655  
Db 362 GAATGTGAGAAAGAACCGCTCTACTATGGCTGGAAGTTCTCTGTTGGGTAGACCCCA 421  
QY 656 ATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTATGCTCGG 715  
Db 422 ACAGGAATTTTAATGC---TGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGCTCTG 478  
QY 716 AAACCTACTGTGGACTTTATCTCGATCAGAACAGAGTGAAGGAGTGGCTAGTTTCT 775  
Db 479 AAACCTACTGTGGAGGACCGCCCGAGAGTCTGAAAAGAGACAAAGGCCCTGGCAGATTTCA 538  
QY 776 TGAGAAGAAATATCAACAGATTAAGCATACATCAGCATCATTCATCTACTCCAGCATA 835  
Db 539 TCCGCAACACCTCTCCACCATCAAGGCTACCTGACCATCCATCTACTACTACAGATGA 598  
QY 836 TAGTGTTTTCCATATTTCTTATACAGAAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAG 895  
Db 599 TGCTCTACCTTTACTCTCTATGACTACAACTGCCTGAGAACTATCAGGAATTTGAATGCC 658  
QY 896 TAGCCAGTGAAGCAGTTCTGCTCTATTGACAAAACCTAGTAAAAATACAGGATATACATG 955  
Db 659 TGGTGAAGGTGCGGCAAGGAGCTTGCC---ACTCTGATGGCAAGGACCATCATATG 715  
QY 956 GCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTTGGGAGCATTTGGATCTATGATT 1015  
Db 716 GCCCAGGAGCTACACATCTATCTGCTGTGGGGGATCTGACGACTGGTCTTATGATC 775  
QY 1016 TGGGCATCAAAATATTGTTTACATCAAAACCTGTGTAGAAAGCTTTTGGCGTGTCTC 1075  
Db 776 AGGGAATCAAAATATTCTTTTACCTTTTGA-ACCTCGGGATACAGGCTTCTTTGGCTTTCTC 834

RESULT 8  
PCT-US96-00995-5  
; Sequence 5, Application PC/TUS9600995  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
; TITLE OF INVENTION: CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00995  
; FILING DATE: 25-JAN-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 927 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..927  
PCT-US96-00995-5

Query Match 11.5%; Score 124; DB 5; Length 927;  
Best Local Similarity 57.9%; Pred. No. 2.1e-29;  
Matches 278; Conservative 0; Mismatches 195; Indels 7; Gaps 3;  
QY 596 GAATGTGGAGAAAGACCGTTCTTTCTATCGGACAAATCATTCGCATCGGACGACCTGA 655  
DB 362 GAATGTGGAGAAAGACCGTTCTTTCTATCGGACAAATCATTCGCATCGGACGACCTGA 421  
QY 656 ATAGCAACTTGTCTCCAAACACTGTGTGAGGAAGTGCATCCAGTCTCTCATGCTCGG 715  
DB 422 ACAGGAATTTTAATGC---TGGCTGTGTGAAAGTGGAGCTTCTCGAGTCCCTGCTCTG 478  
QY 716 AAACCTACTGTGGAGTTTATCTCTAGTCAGAACAGAGTGAAGGAGTGGCTAGTTTCT 775  
DB 479 AAATCTACTGTGGACCGCCAGAGTCTTGAAAGAGACAAAGGCGCTGGCAGATTTCA 538  
QY 776 TGAGAGAAATATCAACAGATTAAGCATACATCAGCATGATTCATATCTCCAGCAT 835  
DB 539 TCGGCAACACCTCTCCACCATCAAGCGCTTACCTGACCATCCACTCATCTACAGATGA 598  
QY 836 TAGTGTTCATATTTCTATACAGAGTAAAGCAAGACCATGAGGAACTGCTCTAG 895  
DB 599 TGCTCTACCTTCTACTCTATGACTACAACTGCTGGAATCTATGAGGAATGGAATGCC 658  
QY 896 TAGCCAGTGAAGCAGTTTCGTGCTATTGACAAAACTAGTAAAAATACAGGTATACATG 955  
DB 659 TGTGGAAGGTGGGCAAGAGGCTTGCC---ACTCTGCATGCGACCAAGTACACATATG 715

QY 956 GCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTTGGATCTATGATT 1015  
DB 716 GCCCAGGAGCTACCAACATCTATCTGCTGCTGGGATCTGACGACTGGTCTTTATGATC 775  
QY 1016 TGGGCATCAATATTCGTTTACATCAACACCACTGTAGAGAACTTTTGGCGGTGCTC 1075  
DB 776 AGGAATCAATATTCCTTTTACCTTTGA-ACCTCGGGATACAGGCTTCTTTGGGCTTTCTC 834  
RESULT 9  
US-08-696-139-3  
; Sequence 3, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hersenberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696.139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gavlo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 921 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..921  
US-08-696-139-3  
Query Match 11.4%; Score 123.4; DB 1; Length 921;  
Best Local Similarity 56.3%; Pred. No. 3.3e-29;  
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;  
QY 555 GATCTCTCTCTGCTTTTCTGCTTGTGTTTCATAGGCCATATCGAATGTGAGAAAGACCG 614  
DB 321 GCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCCGAATGTGAGAAAGACCG 380  
QY 615 TTCTTTTCTATGGAACAATCATTCGATCGGAACAGACCTGATGCAACTTTGTCTCCAA 674  
DB 381 CTCTACCAATGCTGGAACTACCTGCAATTGGCAGACCAACAGAAATTTTGTGCTGG 440

QY 675. AACTGCTGTGAGGAGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGACTTTA 734  
DB 441 G---TGGTGCAAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGGATCTGC 497  
QY 735 TCCTCAGTGCAGAACCAAGAGTGAAGCGAGTGGCTAGTTCCTTGAGAGAAATATCAACCA 794  
DB 498 TCCAGAGTCTGAAAAGAGACCAAGCCCTGGCTGATTTATACCAACACCTCTCCTC 557  
QY 795 GATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTA 854  
DB 558 CATCAAGCATACCTGACGATCCACTCATCTACAGATGATCTCTACCCCTTATTCCTA 617  
QY 855 TACAGAGTAAAGCAAGACCATGAGCACTGTCTCTAGTAGCCAGTGAAGCATGTCG 914  
DB 618 TGATTACAAACTCCCGAGAACATGCTGAGTTGAATAACCTGGCTAAGGCTGCGGTGAA 677  
QY 915 TGCTATTACAAAACTAGTAAATAATACCAAGGTATACATGCGCATGCTCAGAAACCTT 974  
DB 678 AGAAGTTG---CTACACTGTATGGCACCAGTACACATACGCGCCAGGAGCTACAAAT 734  
QY 975 ATACCTAGTCTCTGAGGTGGGAGCATTTGGATCTATGATTTGGGCATCAAAATATTCGTT 1034  
DB 735 CTATCTGCTGTGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAAATATTCCTT 794  
QY 1035 TACAT 1039  
DB 795 CACCT 799

## RESULT 10

US-08-696-139-1  
; Sequence 1, Application US/08696139  
; Patent No. 5672496  
; GENERAL INFORMATION:  
; APPLICANT: Faverman, Jeffrey T.  
; APPLICANT: Greenman, David P.  
; APPLICANT: Hersberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,139  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,258  
; FILING DATE: 16-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-8681  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 276-0756  
; TELEFAX: (317) 276-3861  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1215 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1215  
US-08-696-139-1

Query Match 11.4%; Score 123.4; DB 1; Length 1215;  
Best Local Similarity 56.3%; Pred. No. 3.9e-29;  
Matches 273; Conservative 0; Mismatches 206; Indels 6; Gaps 2;  
QY 555 GATCTCTCCTGCTTCTGCTGTGGTTTCATAGGCCATAATCGAATGTGGAGAAAGACCG 614  
DB 615 GCTCAATATTGATGGCTTACATCTACACCTGGACAAGAACCGAATGTGGAGAAAGACCG 674  
QY 615 TTCTTTCTATCGGAACAAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTCTCCAA 674  
DB 675 CTCTACCAATGCTGGAATACCTGCTGCAATGGCACAGACCCCAACAGAAATTTTGATGCTGG 734  
QY 675 ACATGTGTGAGGAAGGTGATCCAGTTCTCTATGCTCGGAAACCTTACTGTGAGCTTTA 734  
DB 735 G---TGGTGCAAACTGGAGCCTCTACAGACCCCTGCGATGAGACTTACTGTGATCTGC 791  
QY 735 TCCTGAGTCAGAACCAAGTGAAGCGAGTGGCTAGTTCCTTGAGAGAAATATCAACCA 794  
DB 792 TGCAGAGTCTGAAAAGAGAGACCAAGGCCCTGGCTGATTTATACGCAACCACTCTCCTC 851  
QY 795 GATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTA 854  
DB 852 CATCAAGCATACCTGACGATCCACTCATCTACAGATGATCTCTACCCCTTATTCCTA 911  
QY 855 TACAGCAAGTAAAGCAAGACCATGAGGAACCTGCTCTCTAGTAGCCAGTGAAGCATGCG 914  
DB 912 TGATTACAAACTCCCGAGAACATGCTGAGTTGAATAAACCCTGAAGGCTGCGGTGAA 971  
QY 915 TGCTATTGCAAAACTAGTAAATAATACCAATGATGATGATGATGATGATGATGATGAT 974  
DB 972 AGAAGTTG---CTACACTGTATGGCACCAGTACACATACGCGCCAGGAGCTACAAAT 1028  
QY 975 ATACCTAGTCTCTGAGGTGGGAGCATTTGGATCTATGATTTGGGCATCAAAATATTCGTT 1034  
DB 1029 CTATCTGCTGTGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAAAATATTCCTT 1088  
QY 1035 TACAT 1039  
DB 1089 CACCT 1093

## RESULT 11

US-09-011-769A-38  
; Sequence 38, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKE, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38

Query Match 10.1%; Score 109; DB 4; Length 1263;  
Best Local Similarity 54.4%; Pred. No. 1.6e-24;  
Matches 264; Conservative 0; Mismatches 215; Indels 6; Gaps 2;  
QY 555 GATCTCTCTGCTTTCTGCTGTGGTTCTAGGCCATAATCGAATGGAGAAAGAACCG 614  
DB 645 GCTCAATATGATGGCTATACATCTACCTGGACCAAGCCGATTTTGGAGAAAGACTCG 704  
QY 615 TTCTTTCTATGCGAACAATCATTCGATCGGAACAGACCTGAATAGCAACTTTGTCTCAA 674  
DB 705 CTCACCCCTACTGGATCTAGCTGCATTCGACAGACCCCAACAGAAATTTTGATGC--- 761  
QY 675 ACATCGGTGTGAGGAAGGTGCATCCAGTTCCTCATCTCGGAACCTACTGTGGACTTTA 734  
DB 762 TGGTTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGC 821  
QY 735 TCTGTAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAGAAATATCAACCA 794  
DB 822 CGCAGAGTCGAAAGAAACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTC 881  
QY 795 GATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCCTATATTCCTA 854  
DB 882 CATCAAGGCATATCTGACATCCACTCGTACTCCCAATGTATGATCTACCCCTTACTCAT 941  
QY 855 TACAGGAAGTAAAGCAAGACCATGAGGAACCTGTCTTAGTAGCCAGTGAAGCAGTTCG 914  
DB 942 TGCTTACAACTCGGTGAGAACCAATGCTGAGTTGAAATGGCTTGAAGCTACTGTGAA 1001  
QY 915 TGCTATTGACAAACTAGTAAATAATACAGGTATACATGGCCATGGCTTCAGAAACCTT 974  
DB 1002 AGAAGTTCGC---TACTGCACGCAACCAAGTACATATGGCCGCGGAGCTACACAT 1058  
QY 975 ATACCTAGCTCTCGAGGTGGGACGATTTGGATCTATGATTTGGGCATCAATATTCGTT 1034  
DB 1059 CTATCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCT 1118  
QY 1035 TACAT 1039  
DB 1119 CACCT 1123

RESULT 12  
US-09-023-655-1020  
; Sequence 1020, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1020:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1622 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g179933  
US-09-023-655-1020  
Query Match 10.0%; Score 107.6; DB 4; Length 1622;  
Best Local Similarity 55.6%; Pred. No. 5.4e-24;  
Matches 250; Conservative 0; Mismatches 194; Indels 6; Gaps 2;  
QY 590 ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATCGGAAACAATCATTCGATCGGAACAG 649  
DB 686 AGAACCGCATGTGGAGAAAAAATCGTTCCAAGAACCAAACTCCAATTCATCGGCACATG 745  
QY 650 ACTGAATAGCAACTTGTCTCCAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCAT 709  
DB 746 ACCTCAACAGGAATTTAATGTTCA---TGGAACTCCATTCCTAACACCAATGACCCAT 802  
QY 710 GCTCGAAACCTACTGTGGACTTTTATCTCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTA 769  
DB 803 GTGCAGATCACTATCGGGCTCTGCACAGAGTCCGAGAAAGAGACGAAAGCTGTCACTA 862  
QY 770 GTTCTTGAAGAAGAAATATCAACAGATTAAGAGATATACATCAGCATGCTATCATCTCCC 829  
DB 863 ATTTTCAATGAAGCCACCTGAATGAAATCAAGGTTTACATCACCTTCCATTCCTACTCCC 922  
QY 830 AGCATATAGTGTTCATATTCCTATACACGAGTAAAGCAAGCAAGCAAGCAAGCAAGTGT 889  
DB 923 AGATGCTATTGTTCCTATGATATACATCAAACTGCCCACTAACATGAGGACTTGG 982  
QY 890 CTCCTAGTAGCCAGTGAAGCAGTTCTGTCTATTGACAAAACTAGTAAAAATACCAAGTATA 949  
DB 983 CAAAGTTGCAA---AGATTGGCACTGATGTTCTATCACTCGATATGAACCGCTACA 1039  
QY 950 CACATGGCCATGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGAGCGATTGATCT 1009

Db 1040 TCTATGGCCCAATAGATCAACAATTTACCCGATATCAGGTTCTTCTTTAGACTGGGCTT 1099

Qy 1010 ATGATTTGGGCATCAAAATATTCTGTTTACAT 1039

Db 1100 ATGACCTGGGCATCAACACACATTTGCT 1129

## RESULT 13

US-08-860-882A-67

; Sequence 67, Application US/08860882A

; Patent No. 5985281

; GENERAL INFORMATION:

; APPLICANT: TAYLORSON, CHRISTOPHER JOHN

; APPLICANT: EGGEITE, HENDRIKUS JOHANNES

; APPLICANT: TARRAGONA-FIOL, ANTONIO

; APPLICANT: RABIN, BRIAN ROBERT

; APPLICANT: BOYLE, FRANCIS THOMAS

; APPLICANT: HENNAM, JOHN FREDERICK

; APPLICANT: BLAKELY, DAVID CHARLES

; APPLICANT: MARSHAM, PETER ROBERT

; APPLICANT: HEATON, DAVID WILLIAM

; APPLICANT: DAVIES, DAVID HUW

; TITLE OF INVENTION: CHEMICAL COMPOUNDS

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/860,882A

; FILING DATE: JUNE 23, 1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: DONALD J. BIRD

; REGISTRATION NUMBER: 25,323

; REFERENCE/DOCKET NUMBER: 9901/238653

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3027

; TELEFAX: (202) 822-0944

; TELEX: 6174627 CUSH

; INFORMATION FOR SEQ ID NO: 67:

; LENGTH: 999 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-860-882A-67

Query Match 9.9%; Score 107.4; DB 2; Length 999;

Best Local Similarity 54.2%; Pred. No. 4.7e-24;

Matches 263; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

Qy 555 GATCTCTCTGCTTTCTGCTTCTGCTTCTATAGCCATAATCGAATGTGGAGAAACCG 614

Db 387 GCTCAATATGTGCTATCTACACCTGGACCAAGCCGATTTGGAGAAAGACTCG 446

Qy 615 TTCTTCTATGCGAACAATCATGTGATCGGAACAGACCTGAAATAGCAACTTTGTCTCCAA 674

Db 447 CTCACCCATATCGGATCTAGCTGATGGACAGACCCACACAGAATTTGTATGC--- 503

Qy 675 ACACGTGGTGTAGGAGGTGCATCCAGTTCTCATGCTCGGAAACCTACTGTGGACTTGA 734

Db 504 TGGTTGGTGTGAATTTGGAGCCCTCTCGAAACCCCTGTGATGAACTTACTGTGGACCTGC 563

Qy 735 TCTGTAGTCAGAACCAAGAGTGAAGGCGTGTGCTAGTTCTTTGAGAGAAATATCAACCA 794

Db 564 CGCAGAGTCTGAAAGAGAGACCAAGGCCCTGGGCTGATTTTCATCCGCAACAACCTCTCTTC 623

Qy 795 GATTAAGCATACATCAGCATGCAATTCATATCTCCAGCATATAGTGTTCATATTCCTA 854

Db 624 CATCAAGGCATATCTGACAATCCACTCGTACTCCCAATGATGATCTACCCCTTACTCATA 683

Qy 855 TACACGAAGTAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAGTGAAGCAGTTTCG 914

Db 684 TGCTTACAAAATCTCGGTGAGAACAAATGCTGAGTTGAAATGCCCTGCTAAAGCTACTGTGAA 743

Qy 915 TGCTATTGACAAAACTAGTAAAAATACAGATATACACATGCGCCATGGCTCAGAAAACTTT 974

Db 744 AGAATTTGCC---TCACTGACGCGCACCAAGTACATATGCGCCGCGGAGGTACACAAT 800

Qy 975 ATACCTAGCTCTCGAGGTGGGACAGATTCATGATTTGGGCATCAAAATATTCGTT 1034

Db 801 CTATCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTT 860

Qy 1035 TACAT 1039

Db 861 CACCT 865

## RESULT 14

US-09-011-769A-50

; Sequence 50, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; DAVIES, David C.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Pillsbury Madison & Sutro, LLP

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/011,769A

; FILING DATE: 13-Feb-1998

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB96/01975

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9612295.7

; FILING DATE: 12-JUN-1996

; APPLICATION NUMBER: GB 9611019.2

; FILING DATE: 25-MAY-1996

; APPLICATION NUMBER: GB 9516810.0

; FILING DATE: 16-AUG-1995

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 999 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..987







Thu Oct 28 07:16:08 2004

us-09-980-881a-1\_copy\_18\_1097.rnpb

Page 1

GenCore version 5.1.6  
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Run on: October 27, 2004, 09:01:10 ; Search time 569 Seconds

(without alignments)  
9732.531 Million cell updates/sec

Title: US-09-980-881A-1\_COPY\_18\_1097

Perfect score: 1080

Sequence: 1 atgaagcttgagctgtgc.....ttttgcgcgtgtctctaaaaa 1080

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
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8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
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16: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1025.2	94.9	1625	14	Sequence 1, Appli
3	909	84.2	1728	9	US-09-880-107-2396
4	880.8	81.6	1344	16	US-10-115-479-69
5	880.8	81.6	1743	16	US-10-115-479-67
6	854.6	79.1	1272	15	US-10-379-836-1
7	636	58.9	1037	16	US-10-115-479-63
8	593.4	54.9	1132	16	US-10-115-479-65
9	441	40.8	1400	9	US-09-925-302-24
10	441	40.8	1400	10	US-09-925-302-24
11	331.2	30.7	416	9	US-09-960-352-14595
12	282.4	26.1	397	9	US-09-960-352-8425
					Sequence 1, Appli
					Sequence 2396, Ap
					Sequence 69, Appl
					Sequence 67, Appl
					Sequence 1, Appli
					Sequence 63, Appl
					Sequence 65, Appl
					Sequence 24, Appl
					Sequence 24, Appl
					Sequence 14595, A
					Sequence 8425, Ap

13	204	18.9	55827	9	US-09-813-133A-3	Sequence 3, Appli
14	204	18.9	55827	14	US-10-212-877-3	Sequence 3, Appli
15	131	12.1	1547	13	US-10-027-632-265133	Sequence 265133,
16	131	12.1	1547	13	US-10-027-632-265134	Sequence 265134,
17	131	12.1	1547	13	US-10-027-632-265135	Sequence 265135,
18	131	12.1	1547	13	US-10-027-632-265136	Sequence 265136,
19	131	12.1	1547	15	US-10-027-632-265133	Sequence 265133,
20	131	12.1	1547	15	US-10-027-632-265134	Sequence 265134,
21	131	12.1	1547	15	US-10-027-632-265135	Sequence 265135,
22	131	12.1	1547	15	US-10-027-632-265136	Sequence 265136,
23	129.6	12.0	431	9	US-09-917-800A-468	Sequence 468, App
24	107.6	10.0	1254	14	US-10-229-546-3	Sequence 3, Appli
25	107.6	10.0	1622	14	US-10-229-546-1	Sequence 1, Appli
26	107.6	10.0	1622	15	US-10-429-802-21	Sequence 21, Appl
27	107.6	10.0	1622	16	US-10-430-503-12	Sequence 12, Appl
28	107.6	10.0	1622	16	US-10-262-511-71	Sequence 71, Appl
29	107.6	10.0	1622	16	US-10-641-643-1020	Sequence 1020, Ap
30	107.6	10.0	1633	15	US-10-341-434-187	Sequence 187, App
31	107.6	10.0	1740	14	US-10-116-802-95	Sequence 95, Appl
32	104.8	9.7	473	16	US-10-242-535A-42160	Sequence 42160, A
33	104.8	9.7	473	16	US-10-085-783A-42160	Sequence 42160, A
34	101	9.4	1870	9	US-09-910-059-112	Sequence 112, App
35	101	9.4	1870	17	US-10-608-710-3	Sequence 3, Appli
36	101	9.4	2154	9	US-09-910-059-124	Sequence 124, App
37	94.6	8.8	1332	9	US-09-954-456-1141	Sequence 1141, Ap
38	92.8	8.6	1302	17	US-10-477-515-1	Sequence 1, Appli
39	92.8	8.6	1311	13	US-10-200-344-9	Sequence 9, Appli
40	92.8	8.6	1907	18	US-10-757-262-127	Sequence 127, App
41	92.8	8.6	1993	15	US-10-274-639-33	Sequence 33, Appl
42	92.8	8.6	1993	16	US-10-333-574-33	Sequence 33, Appl
43	92.8	8.6	2128	13	US-10-200-344-13	Sequence 13, Appl
44	91.6	8.5	936	15	US-10-106-698-1866	Sequence 1866, Ap
45	88.6	8.2	517	14	US-10-198-846-12472	Sequence 12472, A

## ALIGNMENTS

## RESULT 1

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication NO. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Query Match 94.9%; Score 1025.2; DB 9; Length 1625;  
Best Local Similarity 99.2%; Pred. No. 1.8e+297;  
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1	ATGAAGCTTTGAGCGCTTCAGTCCTTGACCATGTTCTTCTGTGAGCAGCATGTC	60
Db	17	ATGAAGCTTTGAGCGCTTCAGTCCTTGACCATGTTCTTCTGTGAGCAGCATGTC	76
Qy	61	TTGCGCTTTCAGAGTGGCCAAAGTTCTAGCTGCTTTCTTAGAACCTCTAGGCAAGTTCAA	120
Db	77	TTGCGCTTTCAGAGTGGCCAAAGTTCTAGCTGCTTTCTTAGAACCTCTAGGCAAGTTCAA	136
Qy	121	GTTCCTACAGAACTTACTACACATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC	180
Db	137	GTTCCTACAGAACTTACTACACATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC	196

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QY 181 CTTATTGTGAAGAAAAAACAAGTCACATTTTTTTTGTAAATGTCATGATGTCGACAATGTG 240
Db 197 CTTATTGTGAAGAAAAAACAAGTCACATTTTTTTTGTAAATGTCATGATGTCGACAATGTG 256
QY 241 AAAGCCCATTTAAATGTGAGGGAAATTCATGACAGTGTCTTGCTGGCAGAGTGGAAAGAT 300
Db 257 AAAGCCCATTTAAATGTGAGGGAAATTCATGACAGTGTCTTGCTGGCAGAGTGGAAAGAT 316
QY 301 CTTATTCAACAGCAGATTTCAACACACACAGTCAGCCCGCCGAGCCTCCGATCGTACTAT 360
Db 317 CTTATTCAACAGCAGATTTCAACACACACAGTCAGCCCGCCGAGCCTCCGATCGTACTAT 376
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACATGAGAGGAT 420
Db 377 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACATGAGAGGAT 436
QY 421 CCTGATATGCTTCAAAAAATCCACATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 480
Db 437 CCTGATATGCTTCAAAAAATCCACATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 496
QY 481 TTAAGGTTTCTGGAAGAAAGAAACAAACAGCAGCAATGCAATGATGATGATGATGATGATG 540
Db 497 TTAAGGTTTCTGGAAGAAAGAAACAAACAGCAGCAATGCAATGATGATGATGATGATGATG 556
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATAATCGAATG 600
Db 557 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATAATCGAATG 616
QY 601 TGGAGAAAGAACCGTTCTTTCTATCGGAACATCATTCGATCGGACGACCTGATAGC 660
Db 617 TGGAGAAAGAACCGTTCTTTCTATCGGAACATCATTCGATCGGACGACCTGATAGC 676
QY 661 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAC 720
Db 677 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAC 736
QY 721 TACTGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTTCTTGAGA 780
Db 737 TACTGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTTCTTGAGA 796
QY 781 AGAATATCAACAGATTAAGCATATACATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 797 AGAATATCAACAGATTAAGCATATACATGATGATGATGATGATGATGATGATGATGATGATG 856
QY 841 TTTCCATATTTCTTATACAGAAAGTAAAGAGCAAGCAATGAGGAACTGCTCTAGTAGCC 900
Db 857 TTTCCATATTTCTTATACAGAAAGTAAAGAGCAAGCAATGAGGAACTGCTCTAGTAGCC 916
QY 901 AGTGAAGCAGTTCTGCTATTGACAAAACTAGTAAAAATACACAGTATACACATGGCCAT 960
Db 917 AGTGAAGCAGTTCTGCTATTGAGAAAAATAGTAAAAATACACAGTATACACATGGCCAT 976
QY 961 GGCTCAGAAACCTTATACCTAGCTCTCGAGTGGGACGATGATGATGATGATGATGATGATG 1020
Db 977 GGCTCAGAAACCTTATACCTAGCTCTCGAGTGGGACGATGATGATGATGATGATGATGATG 1036
QY 1021 ATCAATATTTCTTTTACA 1038
Db 1037 ATCAATATTTCTTTTACA 1054

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RESULT 2

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US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877

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; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

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Query Match      94.9%; Score 1025.2; DB 14; Length 1625;
Best Local Similarity 99.2%; Pred. No. 1.8e-29;
Matches 1030; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAAGCTTTGACAGCTTGCAGTCTCTGTGATCCCAATGTTCTCTCTCTGAGCAGCATGTC 60
Db 17 ATGAAGCTTTGACAGCTTGCAGTCTCTGTGATCCCAATGTTCTCTCTCTGAGCAGCATGTC 76
QY 61 TTCCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 120
Db 77 TTCCGCTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 136
QY 121 GTTCTACAGATCTTACTACACATATGAGATGTTCTCTGCGACGCGGTAAACAGCTGAC 180
Db 137 GTTCTACAGATCTTACTACACATATGAGATGTTCTCTGCGACGCGGTAAACAGCTGAC 196
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGATCTGATGTCGACAATGTG 240
Db 197 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGATCTGATGTCGACAATGTG 256
QY 241 AAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTGTCTTGTGGCAGAGCTGGAAAGAT 300
Db 257 AAAGCCCATTTAAATGTGAGCGGAAATTCATGCAAGTGTCTTGTGGCAGAGCTGGAAAGAT 316
QY 301 CTTATTCAACAGCAGATTTCCAAACGACACAGCTAGCCCGCCGAGCCTCCGATCGTACTAT 360
Db 317 CTTATTCAACAGCAGATTTCCAAACGACACAGCTAGCCCGCCGAGCCTCCGATCGTACTAT 376
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGGAT 420
Db 377 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATACTGAGAGGAT 436
QY 421 CCTGATATGCTTCAAAAAATCCACATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 480
Db 437 CCTGATATGCTTCAAAAAATCCACATTTGGATCTCTATTGAGAGTACCCACTCTATGTT 496
QY 481 TTAAGGTTTCTGGAAGAAAGAAACAAACAGCAGCAATGCAATGATGATGATGATGATGATG 540
Db 497 TTAAGGTTTCTGGAAGAAAGAAACAAACAGCAGCAATGCAATGATGATGATGATGATGATG 556
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATAATCGAATG 600
Db 557 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATAATCGAATG 616
QY 601 TGGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGATCGGAAACAGACCTGAATAGC 660
Db 617 TGGAGAAAGAACCGTTCTTTCTATGCGAAACATCATTTGATCGATCGGAAACAGACCTGAATAGC 676
QY 661 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAC 720
Db 677 AACTTTGTCTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAAC 736
QY 721 TACTGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTTCTTGAGA 780
Db 737 TACTGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGAGTGGCTAGTTTCTTGAGA 796
QY 781 AGAATATCAACAGATTAAGCATATACATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 797 AGAATATCAACAGATTAAGCATATACATGATGATGATGATGATGATGATGATGATGATGATG 856
QY 841 TTTCCATATTTCTTATACAGAAAGTAAAGAGCAAGCAATGAGGAACTGCTCTAGTAGCC 900

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; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/1115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Query Match
Best Local Similarity 81.6%; Score 880.8; DB 16; Length 1344;
Matches 1031; Conservative 0; Mismatches 7; Indels 126; Gaps 2;

QY 1 ATGAAGCTTTGAGCGCTTGAGCTCCCTGTGACCCATTGTTCTCTCTGTGAGCAGCATGTC 60
Db 31 ATGAAGCTTTGAGCGCTTGAGCTCCCTGTGACCCATTGTTCTCTCTGTGAGCAGCATGTC 90
QY 61 TTCGGGTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 120
Db 91 TTCGGGTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 150
QY 121 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGCGACGCGTAAACGCTGAC 180
Db 151 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGCGACGCGTAAACGCTGAC 210
QY 181 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCACTCTGATGTCGACAATGTG 240
Db 211 CTTATTGTGAAGAAAAAACAAGTCCATTTTTTTGTAATGCACTCTGATGTCGACAATGTG 270
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATCGCAGTGTCTTCTGGCAGAGCGTGAAGAT 300
Db 271 AAAGCCCATTTAAATGTGAGCGGAATTCATCGCAGTGTCTTCTGGCAGAGCGTGAAGAT 330
QY 301 CTTATTCAACAGCAGATTTCACAGACAGCAGTCAGCCCCCGAGCCTCCGCGATCGTACTAT 360
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Db 331 CTTATTCAACAGCAGATTTCACAGACAGCAGTACGCCCCCGAGCCTCCGATCGTACTAT 390
QY 361 GAACAGTATCACTCACTAAATGAATCTATTCTTTGGATAGAAATTTATAAATGAGAGGAT 420
Db 391 GAACAGTATCACTCACTAAATGAATCTATTCTTTGGATAGAAATTTATAAATGAGAGGAT 450
QY 421 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAGTACCCACTCTATGTT 480
Db 451 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAGTACCCACTCTATGTT 510
QY 481 TTAATTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGG 525
Db 511 TTAAGGGTTTCTTTGAGCAGGTTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGG 570
QY 526 ATTGACTGTGGAATCCATGCGCAGAGATGGAATCTCTCTCTGCTTTCTGCTGTTGTTGTTCA 585
Db 571 ATTGACTGTGGAATCCATGCGCAGAGATGGAATCTCTCTCTGCTTTCTGCTGTTGTTGTTCA 630
QY 586 GGCCAT-----AGTTTCTGGAAGAAACAAACAGCCAAAAATGCCATATGG 591
Db 631 GGCCATATACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTGTG 690
QY 592 -----AAT 594
Db 691 GATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGAAAAAGAT 750
QY 595 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAAATCAATGCAATCGGAACAGACCTG 654
Db 751 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAAATCAATGCAATCGGAACAGACCTG 810
QY 655 AATAGCAACTTTGTTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGCTCG 714
Db 811 AATAGGAACCTTTGTTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGCTCG 870
QY 715 GAAACCTACTCTGGACTTTTATCTGAGTCAAGAACAGAGTGAAGGAGTGGCTAGTTTC 774
Db 871 GAAACCTACTCTGGACTTTTATCTGAGTCAAGAACAGAGTGAAGGAGTGGCTAGTTTC 930
QY 775 TTGAGAAAGAAATATCAACAGATTAAGCATATACATCAGCATGCAATTCATCTCCAGAT 834
Db 931 TTGAGAAAGAAATATCAACAGATTAAGCATATACATCAGCATGCAATTCATCTCCAGAT 990
QY 835 ATAGTGTTCCTATATCTTATACAGAGTAAAGCAAGAACCAATGAGGAACCTGTCTCTA 894
Db 991 ATAGTGTTCCTATATCTTATACAGAGTAAAGCAAGAACCAATGAGGAACCTGTCTCTA 1050
QY 895 GTAGCCAGTGAAGCAGTTCTGTTCTATTGACAAAACTAGTAAAAAATACAGGTATACAT 954
Db 1051 GTAGCCAGTGAAGCAGTTCTGTTCTATTGAGAAAAATAGTAAAAAATACAGGTATACAT 1110
QY 955 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGAGCATTTGATCTATGAT 1014
Db 1111 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGAGCATTTGATCTATGAT 1170
QY 1015 TTGGGCATCAATATTCGTTTACA 1038
Db 1171 TTGGGCATCAATATTCGTTTACA 1194
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## RESULT 5

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US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
```

APPLICANT: Zhong, Haibong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIORITY APPLICATION NUMBER: 60/281,136  
PRIORITY FILING DATE: 2001-04-03  
PRIORITY APPLICATION NUMBER: 60/281,863  
PRIORITY FILING DATE: 2001-04-05  
PRIORITY APPLICATION NUMBER: 60/281,906  
PRIORITY FILING DATE: 2001-04-05  
PRIORITY APPLICATION NUMBER: 60/282,934  
PRIORITY FILING DATE: 2001-04-10  
PRIORITY APPLICATION NUMBER: 60/283,657  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,678  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,687  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/283,710  
PRIORITY FILING DATE: 2001-04-13  
PRIORITY APPLICATION NUMBER: 60/284,234  
PRIORITY FILING DATE: 2001-04-17  
PRIORITY APPLICATION NUMBER: 60/285,325  
PRIORITY FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 67  
LENGTH: 1743  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (20)..(1304)

US-10-115-479-67  
Query Match 81.68; Score 880.8; DB 16; Length 1743;  
Best Local Similarity 88.66; Pred. No. 5.6e-254;  
Matches 1031; Conservative 0; Mismatches 7; Indels 126; Gaps 2;

QY 1 ATGAAGCTTTGCGAGCTTGGAGTCTTGTATACCCATTTCTCTCTGTGAGCAGCATGTC 60  
DB 20 ATGAAGCTTTGCGAGCTTGGAGTCTTGTATACCCATTTCTCTCTGTGAGCAGCATGTC 79  
QY 61 TTCGCGTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 80 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 139  
QY 121 GTTCTACAGATCTTACTACACATATGAGATTTCTCTGGCAGCGGTAAACAGCTGAC 180  
DB 140 GTTCTACAGATCTTACTACACATATGAGATTTCTCTGGCAGCGGTAAACAGCTGAC 199  
QY 181 CTTATTGTGAAGAAAAACAGTCCATTTTTTGTAAATGATCTGATGTCGACAATGTG 240  
DB 200 CTTATTGTGAAGAAAAACAGTCCATTTTTTGTAAATGATCTGATGTCGACAATGTG 259

QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATCAGTGTCTTCTGGCAGACGTGGAAGAT 300  
DB 260 AAAGCCCATTTAAATGTGAGCGGAATTCATCAGTGTCTTCTGGCAGACGTGGAAGAT 319  
QY 301 CTTATTCAACAGCAGATTTCCAAACGACACAGTCCGAGCCCGGAGCCCTCGCATCTGATAT 360  
DB 320 CTTATTCAACAGCAGATTTCCAAACGACACAGTCCGAGCCCGGAGCCCTCGCATCTGATAT 379  
QY 361 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACAGAGGCAT 420  
DB 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACAGAGGCAT 439  
QY 421 CCTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAATGACCATCTATGTT 480  
DB 440 CCTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTGAGAAATGACCATCTATGTT 499  
QY 481 TTAA-----AGSTTTCTGAAAAGAACAAACAGCCCAAAATGCCATATGG 525  
DB 500 TTAAGAGGTTTCTTTGAGCAGGTTTCTGAAAAGAACAAACAGCCCAAAATGCCATATGG 559  
QY 526 ATTGACTGTGGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTTGTTGTTTCA 585  
DB 560 ATTGACTGTGGAATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTTGTTGTTTCA 619  
QY 586 GGCCAT----- 591  
DB 620 GGCCATATTAACCTCAATTTCTATGGGATAATAGGGAATATACCAATCTCTGAGGCTTGTG 679  
QY 592 -----AAT 594  
DB 680 GATTTCTATGTTATGCCAGTGGTTAATGTGGATGTTATGACTACTATCGSAAAAAAGAT 739  
QY 595 CGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACATTCATTGCAATCGGAACAGACCTG 854  
DB 740 CGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACATTCATTGCAATCGGAACAGACCTG 799  
QY 655 AATAGCAACTTTGTCTCCAAACACATGTTGTGAGGAGGTGCAATCCAGTTCTCTCATGCTCG 714  
DB 800 AATAGCAACTTTGTCTCCAAACACATGTTGTGAGGAGGTGCAATCCAGTTCTCTCATGCTCG 859  
QY 715 GAAACCTACTGTGGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTTC 774  
DB 860 GAAACCTACTGTGGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGTTTC 919  
QY 775 TTGAGAGAAATATCAACAGATTAAGCATATACATCAGCATGCAATCTACTATCCAGCAT 834  
DB 920 TTGAGAGAAATATCAACAGATTAAGCATATCAACAGATTAAGCATGCAATCTACTATCCAGCAT 979  
QY 835 ATAGTGTCTTCCATATTTCTATACAGAAAGTAAAGCAAAAGACCATGAGGAATGTCTCTTA 894  
DB 980 ATAGTGTCTTCCATATTTCTATACAGAAAGTAAAGCAAAAGACCATGAGGAATGTCTCTTA 1039  
QY 895 GTAGCCAGTGAAGCAGTCTGCTATTTGACAAATCTAGTAAATAATACCAGGTATACACAT 954  
DB 1040 GTAGCCAGTGAAGCAGTCTGCTATTTGAGAAAAATAGTAAAAAATACCAGGTATACACAT 1099  
QY 955 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAGATTGGATCTATGAT 1014  
DB 1100 GGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAGATTGGATCTATGAT 1159  
QY 1015 TTGGGCATCAATATTTCTGTTTACA 1038  
DB 1160 TTGGGCATCAATATTTCTGTTTACA 1183

RESULT 6

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON





PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 63  
LENGTH: 1037  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (41)..(1007)  
US-10-115-479-63

Query Match 58.9%; Score 636; DB 16; Length 1037;  
Best Local Similarity 81.0%; Pred. No. 2.2e-180;  
Matches 841; Conservative 0; Mismatches 5; Indels 192; Gaps 1;

QY 1 ATGAAGCTTTGAGCCTTCAGTCCCTGACGCTTGTACCCATGTTCTCTCTGTGAGCAGCATGTC 60  
DB 41 ATGAAGCTTTGAGCCTTCAGTCCCTGACGCTTGTACCCATGTTCTCTCTGTGAGCAGCATGTC 100  
QY 61 TTGCGGTTCCAGAGTGGGCAAGTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 120  
DB 101 TTGCGGTTCCAGAGTGGGCAAGTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
QY 121 GTTCTACAGAATCTTACTACAAATATGAGATGTTCTCTGCGAGCGGTAAACAGCTGAC 180  
DB 161 GTTCTACAGAATCTTACTACAAATATGAGATGTTCTCTGCGAGCGGTAAACAGCTGAC 220  
QY 181 CTTATTGTGAAGAAAAAAGTCCATTTTTTTTGTAAATGTCATGTCGACATGTC 240  
DB 221 CTTATTGTGAAGAAAAAAGTCCATTTTTTTTGTAAATGTCATGTCGACATGTC 280  
QY 241 AAAGCCATTAAATCTGAGCGGAATCCATGCTGCTGTCGACAGCTGCGAAGAT 300  
DB 281 AAAGCCATTAAATGTGAGCGGAATCCATGCTGCTGTCGACAGCTGCGAAGAT 340  
QY 301 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGTCCGAGCCCTCCGATCGTACTAT 360  
DB 341 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGTCCGAGCCCTCCGATCGTACTAT 400  
QY 361 GAAAGATATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTAATCTGAGAGCAT 420  
DB 401 GAAAGATATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTAATCTGAGAGCAT 460  
QY 421 CCTGATATGCTTACAAATCCACATTTGATCTCTCTTTGAGAGTACCCACTCTATGTT 480  
DB 461 CCTGATATGCTTACAAATCCACATTTGATCTCTCTTTGAGAGTACCCACTCTATGTT 520  
QY 481 TTAAGGTTTCTGGAAGAAACAAACAGCCAAATGCCATATGGATTTGACTGTGGAATC 540  
DB 521 TTAAGGTTTCTGGAAGAAACAAACAGCCAAATGCCATATGGATTTGACTGTGGAATC 569  
QY 541 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATCAATG 600  
DB 570 ----- 569  
QY 601 TGGAGAAAGAACCGTTCTTTCTATGCGAACATCAATTCGACGAGACACCTGAATAGC 660  
DB 570 ----- 569  
QY 661 AACTTTGTCTCAAACACTGGTGTGAGAGGTGTCATCCAGTTCTCTCATCTCGGAACC 720

570 ----- 569  
QY 721 TACTGTGAGCTTTATCTCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTCTTTGAGA 780  
DB 570 -ACTGTGAGCTTTATCTCTGAGTCAGAACCAAGAGTGAAGGAGTGGCTAGTTCTTTGAGA 628  
QY 781 AGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTCCAGCATATAGTG 840  
DB 629 AGAAATATCAACAGATTTAAAGCATATCATCAGCATGCAATTCATCTCCAGCATATAGTG 688  
QY 841 TTTCCATATTTCTATACAGGAAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCC 900  
DB 689 TTTCCATATTTCTATACAGGAAGTAAAGCAAGCAACCATGAGGAAGTCTCTCTAGTAGCC 748  
QY 901 AGTGAAGCAGTTCTGCTATTGACAAAATAGTAAATAACCAAGTATACACATGSCCAT 960  
DB 749 AGTGAAGCAGTTCTGCTATTGAGAAAATTTAGTAAATAACCAAGTATACACATGSCCAT 808  
QY 961 GGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGAGCGATTGGATCTATGATTTGGGC 1020  
DB 809 GGCTCAGAAACCTTATACCTAGCTCCTGGAGTGGGAGCGATTGGATCTATGATTTGGGC 868  
QY 1021 ATCAAAATATTCGTTTACA 1038  
DB 869 ATCAAAATATTCGTTTACA 886

RESULT 8  
US-10-115-479-65  
Sequence 65, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Hailong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Purnak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(1103)
US-10-115-479-65

Query Match 54.9%; Score 593.4; DB 16; Length 1132;
Best Local Similarity 84.9%; Pred. No. 1.5e-167;
Matches 743; Conservative 0; Mismatches 6; Indels 126; Gaps 2;

Qy 1 ATGAGCTTTCAGCCTTCAGTCTCTTACCCATTGTTCTCTGTGAGCAGCATGTC 60
Db 41 ATGAGCTTTCAGCCTTCAGTCTCTTACCCATTGTTCTCTGTGAGCAGCATGTC 100

Qy 61 TTCGGGTTCCAGAGTGGCCAGTCTTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
Db 101 TTCGGGTTCCAGAGTGGCCAGTCTTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160

Qy 121 GTTCTACAGAACTTTACTACAACTATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180
Db 161 GTTCTACAGAACTTTACTACAACTATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220

Qy 181 CTTATTGTGAGAAAAAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 240
Db 221 CTTATTGTGAGAAAAAAGTCCATTTTGTAAATGATCTGATGTCGACAAATGTG 280

Qy 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGCTTCTGGCAGAGCTGGAAGAT 300
Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGCTTCTGGCAGAGCTGGAAGAT 340

Qy 301 CTTATTCAACAGCAGATTTCACAAACGACAGCTAGCCCCCGAGCTCCGCAATCGTACTAT 360
Db 341 CTTATTCAACAGCAGATTTCACAAACGACAGCTAGCCCCCGAGCTCCGCAATCGTACTAT 400

Qy 361 GAACAGTATCACTCAATAATGAATCTATTCTTGGATAGAAATTTATTAATCTGAGAGGAT 420
Db 401 GAACAGTATCACTCAATAATGAATCTATTCTTGGATAGAAATTTATTAATCTGAGAGGAT 460

Qy 421 CCTGATATGCTTACAAAAATCCAAATGGATCTCTCAITTTGAGAGTACCCACTCTATGTT 480
Db 461 CCTGATATGCTTACAAAAATCCAAATGGATCTCTCAITTTGAGAGTACCCACTCTATGTT 520

Qy 481 TTAA-----AGTTTTCGAAAGAACAAACAGCCCAAAATGCCATATGG 525
Db 521 TTAAAGGGTTTCTTGTGAGCAGGTTCTCGAAAAAGAACAGCAGCCCAAAATGCCATATGG 580

Qy 526 ATTGACTGTGGATCCAGCCAGAAATGATCTCTGCTTCTGCTTCTGCTTCTGCTTCTATA 585
Db 581 ATTGACTGTGGATCCAGCCAGAAATGATCTCTGCTTCTGCTTCTGCTTCTGCTTCTATA 640

Qy 586 GGCCTAT----- 591
Db 641 GGCCTATAACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTG 700

Qy 592 -----AAT 594
Db 701 GATTTCTATGTTATGCCGTTGTTAAATGTGGATGTTTATGACTACTCATGGAAGAAAT 760

595 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCATCGGAACAGACCTG 654
Db 761 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCATCGGAACAGACCTG 820

Qy 655 AATAGCAACTTTTGTCTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCG 714
Db 821 AATAGGAACCTTTGCTTCCAAACACTGCTGTGAGGAAGTGCATCCAGTTCTCTCATGCTCG 880

Qy 715 GAAACCTACTGTGAGCTTTTATCTGAGTCAAGACC 749
Db 881 GAAACCTACTGTGAGCTTTTATCTGAGTCAAGAAC 915

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL04
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Query Match 40.8%; Score 441; DB 9; Length 1400;
Best Local Similarity 98.9%; Pred. No. 1.3e-121;
Matches 444; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 590 ATATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAAACAATCATTTGCATCGGAACAG 649
Db 177 AGAATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAAACAATCATTTGCATCGGAACAG 236

Qy 650 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 709
Db 237 ACCTGAATAGCAACTTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 296

Qy 710 GCTCGAAACCTACTGTGAGCTTTTATCTCGAGTCAGAACCCAGAGTGAAGCAGTGGCTA 769
Db 297 GCTCGAAACCTACTGTGAGCTTTTATCTCGAGTCAGAACCCAGAGTGAAGCAGTGGCTA 356

Qy 770 GTTCTTGTGAGAGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATCTACTCCC 829
Db 357 GTTCTTGTGAGAGAAATATCAACAGATTAAGCATACATCAGCATGCATTCATCTACTCCC 416

Qy 830 AGCATATAGTGTTCCTATATACAGAACTTAAAGCAAGCAAGACCATGAGGAACCTGT 889
Db 417 AGCATATAGTGTTCCTATATACAGAACTTAAAGCAAGCAAGACCATGAGGAACCTGT 476

Qy 890 CTCTAGTAGCAGTGAAGCAGTTCGTGCTATTGACAAAACCTAGTAAATAATACAGGTATA 949
Db 477 CTCTAGTAGCAGTGAAGCAGTTCGTGCTATTGACAAAACCTAGTAAATAATACAGGTATA 536

Qy 950 CACATGCCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGAGCGATTGGATCT 1009
Db 537 CACATGCCCATGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGAGCGATTGGATCT 596

Qy 1010 ATGATTTGGGCATCAAAATATTTCGTTTACA 1038

Db 597 ATGATTGGGCATCAAAATATTCGTTTACA 625

RESULT 10

US-09-925-302-24

; Sequence 24, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-302-24

Query Match 40.8%; Score 441; DB 10; Length 1400;

Best Local Similarity 98.9%; Pred. No. 1.3e-121;

Matches 444; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 590 ATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAAATCATTTGTCATCGGAACAG 649

Db 177 AGAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAAATCATTTGTCATCGGAACAG 236

QY 650 ACCTGAATAGCACTTTGCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 709

Db 237 ACCTGAATAGCACTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCTCAT 296

QY 710 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACACAGAGTGAAGCGCAGTGGCTA 769

Db 297 GCTCGGAAACCTACTGTGGACTTTATCCTGAGTCAGAACACAGAGTGAAGCGCAGTGGCTA 356

QY 770 GTTCTTTGAGAGAAATATCAACAGANTTAAAGCATATCAGCATGCATTCATCTCCC 829

Db 357 GTTCTTTGAGAGAAATATCAACAGANTTAAAGCATATCAGCATGCATTCATCTCCC 416

QY 830 AGCATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGCCATGAGGAAGTGT 889

Db 417 AGCATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGCCATGAGGAAGTGT 476

QY 890 CTCTAGTAGCAGTGAAGCAGTGTCTGCTATTGCAAAAACCTAGTAAATAACACAGGTATA 949

Db 477 CTCTAGTAGCAGTGAAGCAGTGTCTGCTATTGCAAAAACCTAGTAAATAACACAGGTATA 536

QY 950 CACATGCCATGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGAGCATTTGATCT 1009

Db 537 CACATGCCATGGCTCAGAAACCTTATACCTAGTCTCTGAGGTGGGAGCATTTGATCT 596

QY 1010 ATGATTTGGGCATCAAAATATTCGTTTACA 1038

Db 597 ATGATTTGGGCATCAAAATATTCGTTTACA 625

RESULT 11

US-09-960-352-14595

; Sequence 14595, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 14595

; LENGTH: 416

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 62-LIB34-032-Q1-E1-H10

US-09-960-352-14595

Query Match 30.7%; Score 331.2; DB 9; Length 416;

Best Local Similarity 87.3%; Pred. No. 7.9e-89;

Matches 363; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 150 GATTGTTCTCTGGCAGCCGGTAAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTT 209

Db 1 GATTGTTCTCTGGCAGCCGGTAAACAGCTGACCTTATTGTGAAGAAAAAACAAGTCCATTT 60

QY 210 TTTTGTAAATGCATCTGATGTCGA CAATGTGAAAGCCCATTTAAATGTGAGCGGAATTC 269

Db 61 TTTTGTGAATGCATCTGATGTAAGCAATGTGAAAGCCCATTTAAATGTGAGCGGAATTC 120

QY 270 ATGCAGTGTCTTCTGGCAGCGTGGAGAGATCTTATTCAACAGCAGATTTCCAACGACAC 329

Db 121 ATTCAGGTCCTGGTGGAAATGTGGAAGATCTTATTCGGCAGCAGACTTCCANTGACAC 180

QY 330 AGTCAGCCCCGAGCTCCGCACTCTATGAAACAGTATCCTCACTAAATGAAATCTA 389

Db 181 CATCAGCCCCGGGCATCTCTCTACTATGACAGTATCCTCACTAAATGAGATCTA 240

QY 390 TTCTTGGATAGAAATTTAATCTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGG 449

Db 241 TTCTTGGATAGAAATTTAATCTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTGG 300

QY 450 ATCTCTATTGAGAAAGTACCCACTCTATCTTTTAAAGTTTCTGGAAGAAACAAACAGC 509

Db 301 ATCTCTATACGAGAAAGTACCCACTTTATGTTTAAAGTTTCTTAAAGAAACAAAGGCG 360

QY 510 CAAAATGTCATATGGAATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTG 565

Db 361 CAAAATGTCATATGGAATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTG 416

RESULT 12

US-09-960-352-8425

; Sequence 8425, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 8425

; LENGTH: 397

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 36-LIB34-005-Q1-E1-A12

US-09-960-352-8425

Query Match

Best Local Similarity 26.1%; Score 282.4; DB 9; Length 397;

Matches 319; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```
QY 1 ATGAAGCTTTGAGAGCTTCTGAGCTTCTGTATCCCATGTTCTTCTGTGAGCAGCATGTC 60
DB 18 ATGAAGCTTTATAGCTTTGGAGTCTTGTGCGCACCGTCTGTTCTGTGGGAGCATGCC 77
QY 61 TTCGGTTTCCAGAGTGGCCAGTTCTAGCTCTCTTCTAGAACCTCTTAGCAAGTTCAA 120
DB 78 TTCGGCTTTTCCAGAGGGCCAGGTTTATCTGCTCTTCTAGAACCTCTCAGGCAAGTTCAA 137
QY 121 GTTCTACAGAATCTTACTACAACATATAGATGTTTCTCTGGCAGCCGGTAACAGCTGAC 180
DB 138 ATTCTGCGAGATGTTACTACAACATACAAGATGTTCTCTGGCAGCCAGTAGCAGTGAA 197
QY 181 CTTATGTGAGAAAAAACAAGTCCATTTTTTTTGTAAATGATCATGTGTCGACAAATGTG 240
DB 198 TATATGTGAAGGGATAGCAAGTCCATTTTTTTTGTGAATGCAATCATGTGTAAGCAATGTG 257
QY 241 AAAGCCCATTTAAATGTGAGCGGAATTCATCCAGTGTCTTCTGGCAGAGCTGGAAGAT 300
DB 258 AAAGCCCATTTAAATGTGAGCGAGAAATTCATTCAGGGTCTGTTGGAAAAATGTGGAAGAT 317
QY 301 CTTATTCAACAGCAGATTTCCAACGACACAGTCAAGCCCGAGCCCTCGCATCTGATCTAT 360
DB 318 CTTATCCGCGCAGCAGCTTCCAATGACACCATCAGCCCCCGGGCATCTCTCTCTACTAT 377
QY 361 GAACAGTATCACTCACTAAA 380
DB 378 GAACAGTATCACTCACTAAA 397

RESULT 13
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Query Match 18.9%; Score 204; DB 9; Length 55827;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 744
DB 48643 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702
QY 745 GAACAGAGTGAAGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 804
DB 48703 GAACAGAGTGAAGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 48762
QY 805 TACATCAGATGATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 864
DB 48763 TACATCAGATGATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 48822
QY 865 AAAAGCAAGACCATGAGGAAGT 888
DB 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 14
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 09/813,133
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Query Match 18.9%; Score 204; DB 14; Length 55827;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 744
DB 48643 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702
QY 745 GAACAGAGTGAAGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 804
DB 48703 GAACAGAGTGAAGCGAGTGGCTAGTTTCTTGAGAAGAAATATCAACAGATTAAAGCA 48762
QY 805 TACATCAGATGATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 864
DB 48763 TACATCAGATGATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGGAAGT 48822
QY 865 AAAAGCAAGACCATGAGGAAGT 888
DB 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 15
US-10-027-632-265133
; Sequence 265133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (1)_(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265133

Query Match      12.1%; Score 131; DB 13; Length 1547;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 744
Db 1417 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 1476
QY 745 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 804
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536
QY 805 TACATCAGCAT 815
Db 1537 TACATCAGCAT 1547
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Search completed: October 27, 2004, 10:39:53  
Job time : 576 secs





QY 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
QY 181 HAREWISPAFLWFIH 197  
DB 181 HAREWISPAFLWFIH 197

## RESULT 2

US-08-277-540-3  
; Sequence 3, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-277-540-3

Query Match 54.7%; Score 197; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8.9e-186;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTAD 60  
DB 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTAD 60  
QY 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180  
QY 181 HAREWISPAFLWFIH 197  
DB 181 HAREWISPAFLWFIH 197

## RESULT 3

US-08-430-787A-3  
; Sequence 3, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-430-787A-3

Query Match 54.7%; Score 197; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 8.9e-186;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTAD 60  
DB 1 MKLCSLAVLPVLFCEQHVFAFQSGVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTAD 60  
QY 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
DB 61 LIVKKQVHFFVNASDVNDVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120  
QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPLYVLKVSKEQTAKNAIWDGCI 180



121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 180

181 HAREWISPAFLWFIGH 197

181 HAREWISPAFLWFIGH 197

RESULT 4

US-08-869-057-2

Sequence 2, Application US/08869057

Patent No. 5985562

GENERAL INFORMATION:

APPLICANT: Morser, Michael J

APPLICANT: Nagashima, MariKO

TITLE OF INVENTION: Method of Detecting Thrombotic Disease

TITLE OF INVENTION: Risk

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Berlex Biosciences Legal Department

STREET: 15049 San Pablo Avenue

CITY: Richmond

STATE: California

COUNTRY: USA

ZIP: 94804-0099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/869,057

FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Washtien, Wendy L

REGISTRATION NUMBER: 36,301

REFERENCE/DOCKET NUMBER: 51509AUSM1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-262-5411

TELEFAX: 510-262-7095

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 423 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE: Plasma

TISSUE TYPE: Plasma

FEATURE:

NAME/KEY: Peptide

LOCATION: 23..401

US-08-869-057-2

Query Match 54.7%; Score 197; DB 2; Length 423;

Best Local Similarity 100.0%; Pred. No. 8.9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 60

DB 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 60

QY 61 LIVKKQVHFFVNASDNDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120

DB 61 LIVKKQVHFFVNASDNDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 180

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 180

QY 181 HAREWISPAFLWFIGH 197

DB 181 HAREWISPAFLWFIGH 197

121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 180

181 HAREWISPAFLWFIGH 197

181 HAREWISPAFLWFIGH 197

RESULT 5

US-09-813-133A-2

Sequence 2, Application US/09813133A

Patent No. 6455294

GENERAL INFORMATION:

APPLICANT: GAN, Weiniu et al

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001173

CURRENT APPLICATION NUMBER: US/09/813.133A

CURRENT FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 386

TYPE: PRT

ORGANISM: Human

US-09-813-133A-2

Query Match 46.7%; Score 168; DB 4; Length 386;

Best Local Similarity 100.0%; Pred. No. 3.2e-157; Mismatches 0; Indels 0; Gaps 0;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 60

DB 1 MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 60

QY 61 LIVKKQVHFFVNASDNDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120

DB 61 LIVKKQVHFFVNASDNDNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY 120

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

QY 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

DB 121 EQYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLVLVKVSQVLAALPRTSRQVQLQNLTTTVEIYVLMQPVTD 168

Db 121 EQYHSLNEIYWIEFITERHPDMLTKIHGSSFEKPYLYVLKVSQKEQ 168

## RESULT 7

US-07-649-591B-1  
; Sequence 1, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton  
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649.591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-649-591B-1

Query Match 8.6%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVL 53  
Db 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVL 31

## RESULT 8

US-08-277-540-1  
; Sequence 1, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA: US/08/277,540  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-277-540-1

Query Match 8.6%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVL 53  
Db 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVL 31

## RESULT 9

US-08-430-787A-1  
; Sequence 1, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91

ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-1

Query Match 8.6%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 FOSGQVLAALPRTSRQVQLNLTYYEIVL 53  
Db 1 FOSGQVLAALPRTSRQVQLNLTYYEIVL 31

RESULT 11  
US-08-277-540-7  
Sequence 7, Application US/08277540  
Patent No. 5474901  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,540  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-277-540-7

Query Match 4.2%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DCGIHAREWISPAFC 191  
Db 172 DCGIHAREWISPAFC 186

RESULT 12  
US-08-430-787A-7  
Sequence 7, Application US/08430787A  
Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-1

Query Match 8.6%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 4.3e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 FOSGQVLAALPRTSRQVQLNLTYYEIVL 53  
Db 1 FOSGQVLAALPRTSRQVQLNLTYYEIVL 31

RESULT 10  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-649-591B-7

Query Match 4.2%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DCGIHAREWISPAFC 191  
Db 172 DCGIHAREWISPAFC 186

ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-7

Query Match 4.2%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DCGIHAREWISAPFC 191  
DB 172 DCGIHAREWISAPFC 186

RESULT 13  
US-09-675-305-6  
Sequence 6, Application US/09675305  
Patent No. 6441153  
GENERAL INFORMATION:  
APPLICANT: Donoho, Gregory  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Nehls, Michael  
APPLICANT: Friedrich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
FILE REFERENCE: LEX-0047-USA  
CURRENT APPLICATION NUMBER: US/09/675,305  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/156,685  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 247  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-675-305-6

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Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 175 WIDCGIHAREWI 186  
DB 190 WIDCGIHAREWI 201

RESULT 14  
US-10-200-344-6  
Sequence 6, Application US/10200344  
Patent No. 6780640  
GENERAL INFORMATION:  
APPLICANT: Donoho, Gregory  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Nehls, Michael  
APPLICANT: Friedrich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and  
FILE REFERENCE: LEX-0047-USA  
CURRENT APPLICATION NUMBER: US/10/200,344  
CURRENT FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: US/09/675,305  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 247  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-200-344-6

Query Match 3.3%; Score 12; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 190 WIDCGIHAREWI 201

RESULT 15  
US-09-675-305-12  
Sequence 12, Application US/09675305  
Patent No. 6441153  
GENERAL INFORMATION:  
APPLICANT: Donoho, Gregory  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Nehls, Michael  
APPLICANT: Friedrich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
FILE REFERENCE: LEX-0047-USA  
CURRENT APPLICATION NUMBER: US/09/675,305  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/156,685  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 350  
TYPE: PRT  
ORGANISM: homo sapiens  
US-09-675-305-12

Query Match 3.3%; Score 12; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 WIDCGIHAREWI 186

Db 190 WIDCGIHAREWI 201

Search completed: October 27, 2004, 01:53:58  
Job time : 21.4492 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:41:12 ; Search time 47.2881 Seconds  
(without alignments)  
2464.743 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 360  
Sequence: 1 MKLCSLAVLPVILFCEQHV.....IKVSTSNPPVEKLPLSLK 360

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1364641 seqs, 323758627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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17: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	197	54.7	423	14	US-10-379-836-17
2	168	46.7	322	15	US-10-115-479-64
3	168	46.7	386	9	US-09-813-133A-2
4	168	46.7	386	14	US-10-212-877-2
5	168	46.7	423	9	US-09-813-133A-4
6	168	46.7	423	14	US-10-212-877-4
7	162	45.0	354	15	US-10-115-479-66
8	162	45.0	428	15	US-10-115-479-68
9	162	45.0	428	15	US-10-115-479-70
10	84	23.3	211	9	US-09-925-302-467
11	84	23.3	211	10	US-09-925-302-467
12	62	17.2	423	14	US-10-379-836-2
13	27	7.5	422	14	US-10-379-836-18

14	26	7.2	422	14	US-10-379-836-16	Sequence 16, Appl
15	12	3.3	210	16	US-10-363-829-401	Sequence 401, Appl
16	12	3.3	247	13	US-10-200-344-6	Sequence 6, Appl
17	12	3.3	315	9	US-09-888-615-60	Sequence 60, Appl
18	12	3.3	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	3.3	434	16	US-10-477-515-2	Sequence 2, Appl
20	12	3.3	437	13	US-10-200-344-10	Sequence 10, Appl
21	12	3.3	437	14	US-10-274-639-12	Sequence 12, Appl
22	12	3.3	437	15	US-10-333-574-12	Sequence 12, Appl
23	12	3.3	437	17	US-10-757-262-128	Sequence 128, Appl
24	11	3.1	118	15	US-10-074-978A-274	Sequence 274, Appl
25	11	3.1	231	15	US-10-074-978A-48	Sequence 48, Appl
26	11	3.1	231	15	US-10-074-978A-50	Sequence 50, Appl
27	11	3.1	231	15	US-10-074-978A-52	Sequence 52, Appl
28	11	3.1	349	15	US-10-074-978A-46	Sequence 46, Appl
29	11	3.1	402	14	US-10-379-836-20	Sequence 20, Appl
30	11	3.1	416	15	US-10-074-978A-266	Sequence 266, Appl
31	11	3.1	417	15	US-10-074-978A-267	Sequence 267, Appl
32	11	3.1	417	15	US-10-074-978A-268	Sequence 268, Appl
33	11	3.1	417	16	US-10-477-515-3	Sequence 3, Appl
34	11	3.1	613	9	US-09-910-059-113	Sequence 113, Appl
35	11	3.1	613	16	US-10-608-710-4	Sequence 4, Appl
36	11	3.1	716	9	US-09-910-059-125	Sequence 125, Appl
37	10	2.8	231	15	US-10-074-978A-54	Sequence 54, Appl
38	10	2.8	310	16	US-10-470-390A-20	Sequence 20, Appl
39	10	2.8	374	9	US-09-888-615-61	Sequence 61, Appl
40	10	2.8	416	15	US-10-074-978A-270	Sequence 270, Appl
41	10	2.8	444	14	US-10-176-306-74	Sequence 74, Appl
42	9	2.5	286	16	US-10-408-765A-1959	Sequence 1959, Ap
43	9	2.5	323	14	US-10-369-493-6610	Sequence 6610, Ap
44	9	2.5	323	14	US-10-369-493-6611	Sequence 6611, Ap
45	9	2.5	417	14	US-10-229-546-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-379-836-17  
; Sequence 17, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; TITLE OF INVENTION: TAFI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 17  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-379-836-17

Query Match	54.7%	Score 197;	DB 14;	Length 423;
Best Local Similarity	100.0%	Pred. No. 2.6e-182;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLATTYEVILWQPVTAD	60	
Db	1	MKLCSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQVQLQNLATTYEVILWQPVTAD	60	
Qy	61	LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY	120	
Db	61	LIVKKQVHFFVNASDVNVKAHLNVSGIPCSVLLADVEDLIQQQISNDTVSPRASASY	120	
Qy	121	EQVHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKPYLYLVKVSQKQTAKNAIWDGCI	180	
Db	121	EQVHSLNEIYSWIEFITERHPDMLTKIHIGSSFEKPYLYLVKVSQKQTAKNAIWDGCI	180	

Qy	181	HARWISPAFCLWFTGH	197
Db	181	HARWISPAFCLWFTGH	197
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US-10-115-479-64			
; Sequence 64, Application US/10115479			
; Publication No. US20040006205A1			
; GENERAL INFORMATION:			
; APPLICANT: Li, Li			
; APPLICANT: Gerlach, Valerie L.			
; APPLICANT: Liu, Xiaohong			
; APPLICANT: Miller, Charles E.			
; APPLICANT: Spytek, Kimberly A.			
; APPLICANT: Zethusen, Bryan D.			
; APPLICANT: Pena, Carol E.A.			
; APPLICANT: Shenoy, Suresh G.			
; APPLICANT: Zhong, Haihong			
; APPLICANT: Smithson, Glenda			
; APPLICANT: Casman, Stacie J.			
; APPLICANT: Boldog, Ferenc L.;			
; APPLICANT: Voss, Edward			
; APPLICANT: Vernet, Corine			
; APPLICANT: MacDougall, John A.			
; APPLICANT: Rastelli, Luca			
; APPLICANT: Anderson, David W.			
; APPLICANT: Zhong, Mei			
; APPLICANT: Mezes, Peter S.			
; APPLICANT: Furtak, Katarzyna			
; APPLICANT: Patturajan, Meera			
; APPLICANT: Burgess, Catherine E.			
; APPLICANT: Maiyanker, Uriel M.			
; APPLICANT: Shimkets, Richard A.			
; APPLICANT: Taupier, Raymond J.			
; APPLICANT: Edinger, Shlomit R.			
; APPLICANT: Mazur, Ann			
; TITLE OF INVENTION: THERAPEUTIC POL			
; FILE REFERENCE: 21402-322 B (Cura 6			
; CURRENT APPLICATION NUMBER: US/10/1			
; CURRENT FILING DATE: 2002-11-18			
; PRIOR APPLICATION NUMBER: 60/281,13			
; PRIOR FILING DATE: 2001-04-03			
; PRIOR APPLICATION NUMBER: 60/281,86			
; PRIOR FILING DATE: 2001-04-05			
; PRIOR APPLICATION NUMBER: 60/281,90			
; PRIOR FILING DATE: 2001-04-05			
; PRIOR APPLICATION NUMBER: 60/282,93			
; PRIOR FILING DATE: 2001-04-10			
; PRIOR APPLICATION NUMBER: 60/283,65			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: 60/283,67			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: 60/283,68			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: 60/283,71			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: 60/284,23			
; PRIOR FILING DATE: 2001-04-17			
; PRIOR APPLICATION NUMBER: 60/285,32			
; PRIOR FILING DATE: 2001-04-19			
; Remaining of SEQ Application data re			
; NUMBER OF SEQ ID NOS: 198			
; SEQ ID NO 64			
; LENGTH: 322			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-115-479-64			

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Db 1 MKLCSLAVLPVILFCEQHVFAFQSGOVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASAYY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASAYY 120  
Qy 121 EQYHSLNEIYSWIEFTITERHPDMLTKIHGSSPEKYPYLVLKVSQKEQ 168  
Db 121 EQYHSLNEIYSWIEFTITERHPDMLTKIHGSSPEKYPYLVLKVSQKEQ 168

RESULT 3  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US2002013719A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 46.7%; Score 168; DB 9; Length 386;  
Best Local Similarity 100.0%; Pred. No. 3.3e-154; Indels 0; Gaps 0;  
Matches 168; Conservative 0; Mismatches 0;

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Db 1 MKLCSLAVLPVILFCEQHVFAFQSGOVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTD 60  
Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASAYY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASAYY 120  
Qy 121 EQYHSLNEIYSWIEFTITERHPDMLTKIHGSSPEKYPYLVLKVSQKEQ 168  
Db 121 EQYHSLNEIYSWIEFTITERHPDMLTKIHGSSPEKYPYLVLKVSQKEQ 168

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US-10-212-877-2  
; Sequence 2, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-212-877-2



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Query Match          46.7%; Score 168; DB 14; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.3e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60

QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168

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; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match          46.7%; Score 168; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60

QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168

RESULT 6
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; Sequence 4, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
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; ORGANISM: Human
US-10-212-877-4

Query Match          46.7%; Score 168; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTYYEIVLWQPVTAD 60

QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
DB 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

QY 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168
DB 121 EOYHSLNEIYSWIEFITERHPDMLTKIHIGSSFYKPYLYLVKVSQKEQ 168

RESULT 7
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
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; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match      45.0%; Score 162; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 2e-148;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCSLAVLPVILFCEQHVFAFGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60
Db 1 MKLCSLAVLPVILFCEQHVFAFGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60

Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKYPVLYLK 162
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKYPVLYLK 162

RESULT 8
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
```

```
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match      45.0%; Score 162; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.4e-148;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLCSLAVLPVILFCEQHVFAFGQVLAALPRTSRQVQLNLTITTYEIVLWQPVTD 60

Qy 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVSGIPCSVLLADVEDLIQQOISNDTVSPRASASY 120

Qy 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKYPVLYLK 162
Db 121 EYHSLNEIYSWIEFITERHPDMLTKIHIGSSFKEKYPVLYLK 162

RESULT 9
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
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;; PRIOR FILING DATE: 2001-04-03  
;; PRIOR APPLICATION NUMBER: 60/281,863  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/281,906  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/282,934  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 70  
;; LENGTH: 428  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-115-479-70

Query Match 45.0%; Score 162; DB 15; Length 428;  
Best Local Similarity 100.0%; Pred. No. 2.4e-148;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTD 60  
  
QY 61 LIVKKQVHFFVNASDVNDVNVKAHLNVGIPCSVLLADVDELIIQQISNDTVSPRASASY 120  
Db 61 LIVKKQVHFFVNASDVNDVNVKAHLNVGIPCSVLLADVDELIIQQISNDTVSPRASASY 120  
  
QY 121 EQVHSLNEIYSWIEFITERHPDMLTKIHIGSSPEKPYLVLK 162  
Db 121 EQVHSLNEIYSWIEFITERHPDMLTKIHIGSSPEKPYLVLK 162

RESULT 10  
US-09-925-302-467  
; Sequence 467, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 467  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-302-467

Query Match 23.3%; Score 84; DB 9; Length 211;  
Best Local Similarity 100.0%; Pred. No. 6.5e-73;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 224 SKHWCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPY 283  
Db 49 SKHWCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPY 108

QY 284 SYTRSKSKDHEELSLVASEAVRAI 307  
Db 109 SYTRSKSKDHEELSLVASEAVRAI 132  
  
RESULT 11  
US-09-925-302-467  
; Sequence 467, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 467  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-302-467

Query Match 23.3%; Score 84; DB 10; Length 211;  
Best Local Similarity 100.0%; Pred. No. 6.5e-73;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 224 SKHWCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPY 283  
Db 49 SKHWCEGASSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSQHI VFPY 108  
  
QY 284 SYTRSKSKDHEELSLVASEAVRAI 307  
Db 109 SYTRSKSKDHEELSLVASEAVRAI 132

RESULT 12  
US-10-379-836-2  
; Sequence 2, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Papio hamadryas  
US-10-379-836-2

Query Match 17.2%; Score 62; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 2.7e-51;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MKLCSLAVLPVILFCEQHVFAFQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTD 60  
  
QY 61 LI 62  
Db 61 LI 62

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RESULT 13
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Query Match          7.5%; Score 27; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 NDTVSPRASASYEQYHSLNIYSWIE 134
Db 107 NDTVSPRASASYEQYHSLNIYSWIE 133

RESULT 14
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Query Match          7.2%; Score 26; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 KNAIWIDCGIHAREWISPAFLWFIG 196
Db 170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 15
US-10-363-829-401
; Sequence 401, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;

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; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Iman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 401
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 102
; OTHER INFORMATION: unknown or other
US-10-363-829-401

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Query Match          3.3%; Score 12; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 175 WIDCGIHAREWI 186
Db 48 WIDCGIHAREWI 59

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Job time : 48.2881 secs

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GenCore version 5.1.6  
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Run on: October 27, 2004, 01:56:38 ; Search time 94.5763 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

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Perfect score: 360  
Sequence: 1 MKLCLAVLPVILVFCQHV.....IKYFTSNPPVKKLPLSLK 360

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues  
Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	197	54.7	1272	US-08-869-057-1	Sequence 1, Appli
2	197	54.7	1749	US-07-649-591B-2	Sequence 2, Appli
3	197	54.7	1749	US-08-277-540-2	Sequence 2, Appli
4	197	54.7	1749	US-08-430-787A-2	Sequence 1, Appli
5	168	46.7	1625	US-09-813-133A-1	Sequence 3, Appli
6	68	18.9	55827	US-09-813-133B-3	Sequence 5, Appli
7	12	3.3	741	US-09-875-305-5	Sequence 5, Appli
8	12	3.3	741	US-10-200-344-5	Sequence 11, Appl
9	12	3.3	1050	US-09-675-305-11	Sequence 11, Appl
10	12	3.3	1050	US-10-200-344-11	Sequence 11, Appl
11	12	3.3	1311	US-09-675-305-9	Sequence 9, Appli
12	12	3.3	1311	US-10-200-344-9	Sequence 9, Appli

13	12	3.3	2128	4	US-09-675-305-13	Sequence 13, Appl
14	12	3.3	2128	4	US-10-200-344-13	Sequence 13, Appl
15	11	3.1	258	4	US-09-270-767-25119	Sequence 25119, A
16	11	3.1	359	4	US-09-513-999C-3571	Sequence 3571, Ap
17	11	3.1	927	2	US-08-782-760-5	Sequence 5, Appli
18	11	3.1	927	5	PCT-US96-00995-5	Sequence 5, Appli
19	11	3.1	999	2	US-08-860-882A-67	Sequence 67, Appl
20	11	3.1	999	4	US-09-011-769A-50	Sequence 50, Appl
21	11	3.1	1053	2	US-08-860-882A-64	Sequence 64, Appl
22	11	3.1	1053	4	US-09-011-769A-46	Sequence 46, Appl
23	11	3.1	1053	4	US-09-463-451-27	Sequence 27, Appl
24	11	3.1	1053	4	US-09-463-451-28	Sequence 28, Appl
25	11	3.1	1059	2	US-08-860-882A-74	Sequence 74, Appl
26	11	3.1	1059	2	US-08-860-882A-77	Sequence 77, Appl
27	11	3.1	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	11	3.1	1059	4	US-09-011-769A-63	Sequence 63, Appl
29	11	3.1	1150	4	US-09-270-767-9829	Sequence 9829, Ap
30	11	3.1	1263	2	US-08-860-882A-56	Sequence 56, Appl
31	11	3.1	1263	4	US-09-011-769A-38	Sequence 38, Appl
32	11	3.1	1284	2	US-08-860-882A-71	Sequence 71, Appl
33	11	3.1	1284	4	US-09-011-769A-55	Sequence 55, Appl
34	11	3.1	1870	3	US-09-171-945-112	Sequence 112, App
35	11	3.1	2154	3	US-09-171-945-124	Sequence 124, App
36	9	2.5	486	4	US-09-248-796A-870	Sequence 870, App
37	9	2.5	1622	4	US-09-023-655-1020	Sequence 1020, Ap
38	8	2.2	873	4	US-09-583-110-2322	Sequence 2322, Ap
39	8	2.2	882	4	US-09-252-991A-11174	Sequence 11174, A
40	8	2.2	918	4	US-09-252-991A-11018	Sequence 11018, A
41	8	2.2	1113	4	US-09-252-991A-11239	Sequence 11239, A
42	8	2.2	1325	3	US-09-412-102-3	Sequence 3, Appli
43	8	2.2	1325	3	US-09-217-787-3	Sequence 3, Appli
44	8	2.2	1347	3	US-09-412-102-1	Sequence 1, Appli
45	8	2.2	1347	3	US-09-217-787-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Moreser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; AUTHORS: Eaton, Dan L.
; AUTHORS: Malloy, Beth E.
; AUTHORS: Tsai, Siao P
; AUTHORS: Henzel, William
; TITLE: Isolation, Molecular Cloning, and Partial
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B
; JOURNAL: J. Biol. Chem.
; VOLUME: 266
; ISSUE: 32
; PAGES: 21833-21838
; DATE: No. 5985562 15-1991
;
US-08-869-057-1
;
Alignment Scores:
Pred. No.: 3.08e-197 Length: 1272
Score: 197.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.72% Indels: 0
DB: 2 Gaps: 0

US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)
Qy 1 MetLysLeuCySerLeuAlaValLeuValProLeuValLeuPheCysGluGlnHisVal 20
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Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 61 TTCGGTTTCAGAGTGCCAGTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAA 120
Qy 41 ValLeuGlnAenLeuThrThrThrTyrGluLeuValLeuThrGlnProValThrAlaAsp 60
Db 121 GTTCTACAGATCTTACTACAACTATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 180
Qy 61 LeuLeuValLysLysGlnValHisPhePheValAenAlaSerAspValAspVal 80
Db 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAAATGTG 240
Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100
Db 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGACGATGTTCTGCTGGCAGACGTGGAAGAT 300
Qy 101 LeuLeuGlnGlnGlnLeuSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 301 CTTATTCAACAGCAGATTTCACACACACAGCTGACGCCCGGAGCTCCGCACTCGTACTAT 360
Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheLeuThrGluArgHis 140
Db 361 GAACAGTATCACTCACTAAATGAATATTTCTTGGATAGAAATTTATAACTGAGAGGAT 420
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 421 CCTGATGCTTACAAAAATCCACATTTGATTCCTCATTTTGAGAGTACCCACTCTATGTT 480
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIle 180
Db 481 TTTAAAGGTTTCTGAAAAAGAACAAACGCCAAAAATGCCATATGATGATGCTGTGAATC 540
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db 541 CATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTGTTTCATAGGCCAT 591

RESULT 2
US-07-649-591B-2
; Sequence 2, Application US/07649591B
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; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: hybridization probe
; LOCATION: 133 to 178
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: potential clip site
; LOCATION: 380 to 382
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: 41 to 106
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
US-07-649-591B-2
Alignment Scores:
Pred. No.: 4.22e-197 Length: 1749
Score: 197.00 Matches: 197
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.72% Indels: 0
DB: 1 Gaps: 0

US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)
Qy 1 MetLysLeuCySerLeuAlaValLeuValProLeuValLeuPheCysGluGlnHisVal 20
Db 41 ATGAGCTTTTCAGACCTTGCAGTCTTGTACCCATTGTTCTCTCTGTGACGACATGTC 100
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTCGCGTTTCAGAGTGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAA 160
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QY 41 ValLeuGlnAsnLeuThrThrTyrGluLeuValLeuValLeuProValThrAlaAsp 60  
DB 161 GTTCTACAGATCTTACTACATATGATGATTTCTCTGGCAGCCGTAACAGCTGAC 220  
QY 61 LeuileValLysLysGlnValHisPheValAsnAlaSerAspValAspVal 80  
DB 221 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAATGCACTCTGATCGACAATGTG 280  
QY 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
DB 281 AAAGCCCATTTAAATGTGAGCGAATTCATGCGAGTCTTGTGCGACAGCTGGAAGAT 340  
QY 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
DB 341 CTTATTCAACAGAGATTTTCCACAGACACAGTCAGCCCGGAGCTCCGCATCGTACTAT 400  
QY 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTyrPheGluPheIleThrGluArgHis 140  
DB 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460  
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
DB 461 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTATTGAGAAGTACCCTCTATGTT 520  
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheIleAspCysGlyIle 180  
DB 521 TTAAGGTTTCTGGAAGAAAGAACACAGCCAAATGCCATATGGATGACTGTGGAAATC 580  
QY 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 197  
DB 581 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGGTTCATAGGCCAT 631

## RESULT 3

US-08-277-540-2  
; Sequence 2, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-277-540-2

Alignment Scores:  
Pred. No.: 4, 22e-197 Length: 1749  
Score: 197.00 Matches: 197  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 54.72% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)

QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
DB 41 ATGAAGCTTTGCAGCCTTGCAGTCTTGTACCCATTGTTCTTCTGTGAGCAGCATGTC 100  
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
DB 101 TTTCGGGTTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 160  
QY 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
DB 161 GTTCTACAGAACTTCTTACTACAACTATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 220  
QY 61 LeuileValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
DB 221 CTTATTGTGAGAAAAACAAGTCCATTTTTTTGTAATGCACTCTGATCGACAATGTG 280  
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
DB 281 AAAGCCCATTTAAATGTGAGCGAATTCATGCTAGTCTTCTCTGGCAGACGTGGAAGAT 340  
QY 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
DB 341 CTTATTCAACAGCAGATTTTCCAAACAGACACAGTCAGCCCGGAGCTTCCGCATCGTACTAT 400  
QY 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTyrPheGluPheIleThrGluArgHis 140  
DB 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAACTGAGAGGCAT 460  
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
DB 461 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCATTTTGAAGAAGTACCCTCTATGTT 520  
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheIleAspCysGlyIle 180  
DB 521 TTAAGAAGTTTCTGGAAGAAAGAACACAGCCAAATGCCATATGGATGACTGTGGAAATC 580  
QY 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheIleGlyHis 197  
DB 581 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGGTTCATAGGCCAT 631

## RESULT 4

US-08-430-787A-2  
; Sequence 2, Application US/08430787A  
; Patent No. 553674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 553674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 4,228-197 Length: 1749  
Score: 197.00 Matches: 197  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 54.72% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-2 (1-360) x US-08-430-787A-2 (1-1749)

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Db      41 ATGAAGCTTTGAGCGCTTGACGTCCTTGACCATTTGTTCTCTCTGTGAGCAGCATGTC 100

Qy      21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db      101 TTCGGGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160

Qy      41 ValLeuGlnAsnLeuThrThrThrGluIleValLeuThrGlnProValThrAlaAsp 60
Db      161 GTTCTACAGAATCTTACTACACATATGAGATGTTCTCTGCGACCGGTAAACAGCTGAC 220

Qy      61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Db      221 CTTATTGTGAAGAAAACAAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAAATGTG 280

Qy      81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db      281 AAAGCCCATTTAAATGTAGCGGAATTCATGCGAGTGTCTTCTGCGCAGACGCTGGAAGAT 340

Qy      101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db      341 CTTATTCAACAGCAGATTTCACACACACAGTACGCCCCCGAGCTCCGCGATCGTACTAT 400

Qy      121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db      401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 460
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Qy      141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
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Qy      161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db      521 TTAAGGTTTCTGAAAAGAACAAACAGCCAAAATGCCATATGATGATGCTGGAATC 580

Qy      181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db      581 CATGCCAGAGAATGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 631
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#### RESULT 5

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 1,14e-166 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

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Qy      21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
Db      77 TTCGGGTTTCAGAGTGGCCAAAGTTCTAGCTCTCTTCTAGAACCTCTAGGCAAGTTCAA 136

Qy      41 ValLeuGlnAsnLeuThrThrThrGluIleValLeuThrGlnProValThrAlaAsp 60
Db      137 GTTCTACAGAATCTTACTACACATATGAGATGTTCTCTGCGACCGGTAAACAGCTGAC 196

Qy      61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Db      197 CTTATTGTGAAGAAAACAAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACAAATGTG 256

Qy      81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db      257 AAAGCCCATTTAAATGTAGCGGAATTCATGCGAGTGTCTTCTGCGCAGATGTGGAAGAT 316

Qy      101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db      317 CTTATTCAACAGCAGATTTCACACACACAGTACGCCCCCGAGCTCCGCGATCGTACTAT 376

Qy      121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db      377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 436

Qy      141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
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Db 437 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAGAGTACCCACTCTATGTT 496  
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Db 497 TTTAAAGGTTTCTGGAAGAAACAACG-AGCCAAAAATGCCATATGATGGTGTGGAAT 555  
Qy 180 ehialaArgGluTrrPilleSerProAlaPheCysLeuTrrPheIleGlyHisAsnArgMe 200  
Db 556 CCATGCCAGAGAAATGGAATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATAATCGAAT 615  
Qy 200 tTrrArgLysAsnArgSerPheTrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSe 220  
Db 616 GTGGAGAAAGAACCGTTCTTCTATCGGAACAATCATTCATCGCAACAGACCTGAATAG 675  
Qy 220 r-AsnPheVal-SerLysHisTrrPilleSerGlyGluGlyAlaSerSerSerCysSerGlu 239  
Db 676 -GAACCTTTC- TTCCAAACACATGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAA 733  
Qy 240 ThrTrrCysGlyLeuTrrProGluSerGluProGluValLysAlaValAlaSerPheLeu 259  
Db 734 ACTACTGTGGACTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTTCTTG 793  
Qy 260 ArgArgAsnIleAsnGlnIleLysAlaTrrIleSerMetHisSerTrrSerGlnHisIle 279  
Db 794 AGAAGAAATATCAACAGATTAAGCATATACATCAGCATGCATTCATCTCCAGCATATA 853  
Qy 280 ValPheProTrrSerTrrThrArgSerLysSerLysAspHisGlyGluLeuSerLeuVal 299  
Db 854 GTGTTTCCATATCTCTATACAGAGTAAAGCAAGAACCAAGACCATGAGGAACCTGCTCTAGTA 913  
Qy 300 AlaSerGluAlaValArgAlaIle 307  
Db 914 GCCAGTGAAGCAGTTCGTGCTATT 937

## RESULT 6

US-09-813-133A-3  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE OF INVENTION: US THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3

Alignment Scores:  
Pred. No.: 4,15e-60 Length: 55827  
Score: 68.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 18.89% Indels: 0  
Gaps: 4

US-09-980-881A-2 (1-360) x US-09-813-133A-3 (1-55827)

Qy 229 GluGluGlyAlaSerSerSerSerGluThrTrrCysGlyLeuTrrProGluSer 248  
Db 48643 GAGGAAGTGCATCCAGTTCTCTATGCTCGAAACCTACTGTGAGCTTTATCTGAGTCA 48702  
Qy 249 GluProGluValLysAlaValAlaSerPheLeuArgHisIleAsnGlnIleLysAla 268  
Db 48703 GAACCAAGTGAAGGAGTGGTGTGTTCTTTCAGAGAAATATCAACCAAGATTAAGCA 48762  
Qy 269 TyrIleSerMetHisSerTrrSerGlnHisIleValPheProTrrSerTrrThrArgSer 288

Db 48763 TACATCAGCATGCAATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGAGT 48822  
Qy 289 LysSerLysAspHisGlyGluLeu 296  
Db 48823 AAAAGCAAGACCATGAGGAACTG 48846  
RESULT 7  
US-09-675-305-5  
; Sequence 5, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-675-305-5

Alignment Scores:  
Pred. No.: 0.00382 Length: 741  
Score: 12.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.33% Indels: 0  
Gaps: 4

US-09-980-881A-2 (1-360) x US-09-675-305-5 (1-741)

Qy 175 TrpIleAspCysGlyIleHisAlaArgGluTrrIle 186  
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGATT 603

## RESULT 8

US-10-200-344-5  
; Sequence 5, Application US/10200344  
; Patent No. 6780640  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 741  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-200-344-5

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Alignment Scores:
Pred. No.: 0.00382 Length: 741
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-5 (1-741)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 9
US-09-675-305-11
; Sequence 11, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-11
Alignment Scores:
Pred. No.: 0.00539 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-11 (1-1050)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 10
US-10-200-344-11
; Sequence 11, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-11
Alignment Scores:
Pred. No.: 0.00539 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-11 (1-1050)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 11
US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-9
Alignment Scores:
Pred. No.: 0.00672 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-9 (1-1311)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 12
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: Lex-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-9
Alignment Scores:
Pred. No.: 0.00672 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-9 (1-1311)
Qy 175 TptleAspCysGlyIleHisAlaArgGluTrpIle 186
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603
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; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1311  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-200-344-9

Alignment Scores:  
Pred. No.: 1311 Length: 1311  
Score: 0.00672  
Percent Similarity: 12.00% Matches: 12  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
Indels: 0  
DB: 3.33% Gaps: 0

US-09-980-881A-2 (1-360) x US-10-200-344-9 (1-1311)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 568 TGGATAGACTGTGGTATTTCATCCAGAGAATGGATT 603

RESULT 13  
US-09-675-305-13  
; Sequence 13, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 2128  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-675-305-13

Alignment Scores:  
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Score: 0.0109  
Percent Similarity: 12.00% Matches: 12  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
Indels: 0  
DB: 3.33% Gaps: 0

US-09-980-881A-2 (1-360) x US-09-675-305-13 (1-2128)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 933 TGGATAGACTGTGGTATTTCATCCAGAGAATGGATT 968

RESULT 14  
US-10-200-344-13  
; Sequence 13, Application US/10200344  
; Patent No. 6780640  
; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 2128  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-200-344-13

Alignment Scores:  
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Score: 0.0109  
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Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
Indels: 0  
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US-09-980-881A-2 (1-360) x US-10-200-344-13 (1-2128)

Qy 175 TptileAspCysGlyIleHisAlaArgGluTrpIle 186  
Db 933 TGGATAGACTGTGGTATTTCATCCAGAGAATGGATT 968

RESULT 15  
US-09-270-767-25119  
; Sequence 25119, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25119  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-25119

Alignment Scores:  
Pred. No.: 258 Length: 258  
Score: 0.0151  
Percent Similarity: 11.00% Matches: 11  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 100.00% Mismatches: 0  
Indels: 0  
DB: 3.06% Gaps: 0

US-09-980-881A-2 (1-360) x US-09-270-767-25119 (1-258)

Qy 179 GlyIleHisAlaArgGluTrpIleSerProAla 189  
Db 127 GGCATCCAGCCCGCGAATGGATCAGCCCCGCG 159

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Job time : 122.576 secs



GenCore version 5.1.6  
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Searched: 3413475 seqs, 2563800928 residues  
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Database : Published Applications NA:\*

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- 6: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW PUB.seq:\*
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- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodata/2/pubpna/US09D\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*
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- 16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/prodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/prodata/2/pubpna/US11\_NEW PUB.seq:\*
- 20: /cgn2\_6/prodata/2/pubpna/US60\_NEW PUB.seq:\*
- 21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	197	54.7	1728	9	US-09-880-107-2396	Sequence 2396, Ap
2	168	46.7	1037	16	US-10-115-479-63	Sequence 63, Appl
3	168	46.7	1625	9	US-09-813-133A-1	Sequence 1, Appl
4	168	46.7	1625	14	US-10-212-877-1	Sequence 1, Appl
5	162	45.0	1132	16	US-10-115-479-65	Sequence 65, Appl
6	162	45.0	1344	16	US-10-115-479-69	Sequence 69, Appl
7	162	45.0	1743	16	US-10-115-479-67	Sequence 67, Appl
8	84	23.3	1400	9	US-09-925-302-24	Sequence 24, Appl
9	84	23.3	1400	10	US-09-925-302-24	Sequence 24, Appl
10	68	18.9	55827	9	US-09-813-133A-3	Sequence 3, Appl
11	68	18.9	55827	14	US-10-212-877-3	Sequence 3, Appl
12	62	17.2	1272	15	US-10-379-836-1	Sequence 1, Appl
13	43	11.9	1547	13	US-10-027-632-265133	Sequence 265133,
14	43	11.9	1547	13	US-10-027-632-265134	Sequence 265134,
15	43	11.9	1547	13	US-10-027-632-265135	Sequence 265135,
16	43	11.9	1547	13	US-10-027-632-265136	Sequence 265136,
17	43	11.9	1547	15	US-10-027-632-265133	Sequence 265133,
18	43	11.9	1547	15	US-10-027-632-265134	Sequence 265134,
19	43	11.9	1547	15	US-10-027-632-265135	Sequence 265135,
20	43	11.9	1547	15	US-10-027-632-265136	Sequence 265136,
21	19	5.3	60	10	US-09-908-975-8511	Sequence 8511, Ap
22	17	4.7	416	9	US-09-960-352-14595	Sequence 14595, A
23	16	4.4	65	10	US-09-908-975-26009	Sequence 26009, A
24	14	3.9	431	9	US-09-917-800A-468	Sequence 468, App
25	13	3.6	65	10	US-09-908-975-25938	Sequence 25938, A
26	12	3.3	741	13	US-10-200-344-5	Sequence 5, Appl
27	12	3.3	948	9	US-09-888-615-1	Sequence 1, Appl
28	12	3.3	1050	13	US-10-200-344-11	Sequence 11, Appl
29	12	3.3	1187	14	US-10-198-846-13457	Sequence 13457, A
30	12	3.3	1295	17	US-10-363-829-148	Sequence 148, App
31	12	3.3	1302	17	US-10-477-515-1	Sequence 1, Appl
32	12	3.3	1311	13	US-10-200-344-9	Sequence 9, Appl
33	12	3.3	1907	18	US-10-757-262-127	Sequence 127, App
34	12	3.3	1993	15	US-10-274-639-33	Sequence 33, Appl
35	12	3.3	1993	16	US-10-333-574-33	Sequence 13, Appl
36	12	3.3	2128	13	US-10-200-344-13	Sequence 3042, Ap
37	11	3.1	230	14	US-10-060-036-3042	Sequence 3068, Ap
38	11	3.1	230	14	US-10-060-036-3068	Sequence 3096, Ap
39	11	3.1	230	14	US-10-060-036-3131	Sequence 3131, Ap
40	11	3.1	230	14	US-10-060-036-3150	Sequence 3150, Ap
41	11	3.1	230	14	US-10-060-036-3153	Sequence 3153, Ap
42	11	3.1	230	14	US-10-060-036-3164	Sequence 3164, Ap
43	11	3.1	230	14	US-10-060-036-3168	Sequence 3168, Ap
44	11	3.1	230	14	US-10-060-036-3175	Sequence 3175, Ap
45	11	3.1	230	14	US-10-060-036-3175	Sequence 3175, Ap

ALIGNMENTS

RESULT 1  
US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Barci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396
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```
Alignment Scores:
Pred. No.:      6,21e-195      Length:      1728
Score:          197.00         Matches:      197
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:     54.72%        Indels:         0
DB:              9            Gaps:           0
```

US-09-980-881A-2 (1-360) x US-09-880-107-2396 (1-1728)

```
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 20 ATGAAGCTTTGAGGCTTGCAGCTCTTGACCATTTGTTCTTCTGTGAGCAGCATGTC 79
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 80 TTCGGGTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 139
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 140 GTTCTACAGAACTTACTACAACTATGAGATTTGTTCTGGCAGCCGGTAACAGCTGAC 199
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 200 CTTATTTGAGAAAAACAGTCCATTTTGTAAATGATCTGATGTCGACATGTG 259
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 260 AAAGCCCATTTAAATGTGAGCGGAATTCATGCACTGTTCTGTCGACAGCTGGAAGAT 319
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 320 CTTATTCAACAGCAGATTTCCAAACACACAGTCCAGCCCGAGCTCCGCATCGTACTAT 379
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 380 GAACAGTATCACTCAATAAGTAATCTATTCTGGATAGAAATTTATACTGAGAGGAT 439
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 440 CCTGATATGCTTACAAAAATCCACATTTGGATCCCTCATTTGAGAGTACCCACTCTATGTT 499
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 500 TTAAGGTTTCTGGAAAGAAACAAACAGCCAAAAATGCCAATATGATGACTGTGGAATC 559
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db 560 CATGCCAGAGATGGATCTCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAT 610
```

## RESULT 2

US-10-115-479-63

Sequence 63, Application US/10115479

Publication No. US20040006205A1

GENERAL INFORMATION:

APPLICANT: Li, Li

APPLICANT: Gerlach, Valerie L.

APPLICANT: Liu, Xiaohong

APPLICANT: Miller, Charles E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Zerhusen, Bryan D.

APPLICANT: Pena, Carol E.A.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Zhong, Haihong

APPLICANT: Smithson, Glenda

APPLICANT: Casman, Stacie J.

APPLICANT: Boldog, Ferenc L.;

```
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera E.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD.
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 69/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63
```

```
Alignment Scores:
Pred. No.:      6,29e-165      Length:      1037
Score:          168.00         Matches:      168
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:    0
Query Match:     46.67%        Indels:         0
DB:              16            Gaps:           0
```

US-09-980-881A-2 (1-360) x US-10-115-479-63 (1-1037)

```
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 41 ATGAAGCTTTGAGGCTTGCAGCTCTTGACCATTTGTTCTTCTGTGAGCAGCATGTC 100
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 101 TTCGGGTTTCAGAGTGGCCAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAACTTACTACAACTATGAGATTTGTTCTTCTGCGCAGCCGGTAACAGCTGAC 220
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
```

Db 221 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATCGACAATGTG 280  
Qy 81 LysAlaHisLeuAsnValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 281 AAAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTCTGCGCAGACGTGGAAGAT 340  
Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGCAGATTTTCCAAACACACAGTCAGCCCCGAGCCTCGCATCTGACTAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 401 GAACAGTATCACTCACTAAATGAATATTCTTGTAGATAATTTATAACTGAGAGGCAT 460  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCACATCGGATCCTCATTTTGAGAAGTACCACCTCTATGTT 520  
Qy 161 LeuLysValSerGlyLysGluGln 168  
Db 521 TTAAGGGTTTCTGGAAGAAAGACAA 544

## RESULT 3

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1

## GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

## Alignment Scores:

Pred. No.: 9.6e-165 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAGCTTTGAGCCTTGAGTCTGTGTACCCATTGTTCTCTGTGAGCAGCATGTC 76  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTCGCGTTTCAGAGTGCGCAAGTTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 136  
Qy 41 ValLeuGlnAsnLeuThrThrThrThrGluIleValLeuTrpGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGAAATCTTACTACACATATGAGATGTTCTCTGGCAGCGGTAACAGCTGAC 196  
Qy 61 LeuileValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80  
Db 197 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAATGTG 256  
Qy 81 LysAlaHisLeuAsnValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTTGTGCGCAGATGTGGAAGAT 316

Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTCAACAGCAGATTTTCCAAACACACAGTCAAGCCCCGAGCCTCGCATCTACTAT 376  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATATTCTTGTAGATAATTTATAACTGAGAGGCAT 436  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CCTGATATGCTTACAAAAATCCACATTTGGAATCCTCATTTGAGAAGTACCACCTCTATGTT 496  
Qy 161 LeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyVal 180  
Db 497 TTAAGGGTTTCTGGAAGAAAGACAAAGC-AGCCAAAAATGCCATATGGATTGACTGTGGAAT 555  
Qy 180 eHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMe 200  
Db 556 CCATGCCAGAGAAATGGATCTCTCCTGCTTTCTGCTTGTGTTTCATAGGCCATTAATCGAAT 615  
Qy 200 tTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSe 220  
Db 616 GTGAGAAAGAACCGTCTCTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAG 675  
Qy 220 r-AsnPheVal-SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGlu 239  
Db 676 -GAACTTTGC-TTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAA 733  
Qy 240 ThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeu 259  
Db 734 ACCTACTGTGACTTTATCTCTGAGTCAGAACAGGAAGTGAAGGCAGTGGTAGTTCTTCTG 793  
Qy 260 ArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIle 279  
Db 794 AGAAGAAATATCAACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATA 853  
Qy 280 ValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuVal 299  
Db 854 GTGTTTCCATATTCTCTATACAGAAAGTAAAGCAAGCCATGAGGAACTGTCTCTAGTGA 913  
Qy 300 AlaSerGluAlaValArgAlaIle 307  
Db 914 GCCAGTGAAGCAGTTCGTGCTATT 937

## RESULT 4

US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1

## GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

## Alignment Scores:

Pred. No.: 9.6e-165 Length: 1625  
Score: 168.00 Matches: 304  
Percent Similarity: 98.06% Conservative: 0  
Best Local Similarity: 98.06% Mismatches: 3  
Query Match: 46.67% Indels: 6  
DB: 14 Gaps: 0





Db 41 ATGAGCTTTGAGCCTTGAGTCTGTGTACCAATGTTCTCTCTGTGAGCAGCATGTC 100  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTGCGGTTTCAGAGTGGCCAAAGTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 160  
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAsp 60  
Db 161 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGTGCAT 220  
Qy 61 LeuLeValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 221 CTTATTGTGAGAAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATCGACATGTC 280  
Qy 81 LysAlaHisLeuAsnValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 281 AAAGCCCATTTAAATGTAGCGGAATTCATGAGTGTCTTGTGCGACAGTGGAGAT 340  
Qy 101 LeuLeGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 341 CTTATTCAACAGACAGATTTCCACGACACAGTCAGCCCCCGAGCTCCGCATCGTACTAT 400  
Qy 121 GluGlnTyrHisSerLeuAsnGluLeTyrSerTrpIleGluPheLeThrGluArgHis 140  
Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAACTGAGAGCAT 460  
Qy 141 ProAspMetLeuThrLysLysLeHisLleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAGAAAGTACCACATCTATGTT 520  
Qy 161 LeuLys 162  
Db 521 TTAAG 526

## RESULT 6

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Sytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard J.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; PRIOR FILING DATE: 2002-11-18  
; CURRENT APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores:  
Pred. No.: 143e-158 Length: 1344  
Score: 162.00 Matches: 162  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.00% Indels: 0  
DB: 16 Gaps: 0  
US-09-980-881A-2 (1-360) x US-10-115-479-69 (1-1344)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 31 ATGAGCTTTGAGCCTTGAGTCTTGTACCAATGTTCTCTCTGTGAGCAGCATGTC 90  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 91 TTGCGGTTTCAGAGTGGCCAAAGTCTAGCTGCTCTTCTAGAACCTCTAGGCAAGTTCAA 150  
Qy 41 ValLeuGlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAsp 60  
Db 151 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGTGCAT 210  
Qy 61 LeuLeValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 211 CTTATTGTGAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATCGACATGTC 270  
Qy 81 LysAlaHisLeuAsnValSerGlyLeProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 271 AAAGCCCATTTAAATGTAGCGGAATTCATGAGTGTCTTGTGCGACAGCGTGAAGAT 330  
Qy 101 LeuLeGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 331 CTTATTCAACAGACAGATTTCCAAACGACACAGTCAGCCCCCGAGCTCCGCATCGTACTAT 390  
Qy 121 GluGlnTyrHisSerLeuAsnGluLeTyrSerTrpIleGluPheLeThrGluArgHis 140  
Db 391 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATAACTGAGAGCAT 450  
Qy 141 ProAspMetLeuThrLysLysLeHisLleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 451 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAGAAAGTACCACATCTATGTT 510  
Qy 161 LeuLys 162  
Db 511 TTAAG 516



DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243

DB 257 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 316

QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263

DB 317 CTTTATCTCTGAGTCAGAACAGAGTGAAGGAGTGGCTAGTTCTTGAGAGAAATATC 376

QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283

DB 377 AACCCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 436

QY 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303

DB 437 TCCATATACACGAAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCCAGTGAAGCA 496

QY 304 ValArgAlaIleAsp-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323

DB 497 GTTCGTGCTATTGA-GAAAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGA 555

QY 323 uThrLeuTyrLeuAlaProGlyGlyGlyAspTrrpIleTyrAspLeuGlyIleLysTyr 343

DB 556 AACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAATA 615

QY 343 rSerPheThr 346

DB 616 TTCGTTTACA 625

RESULT 9

US-09-925-302-24

; Sequence 24, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-302-24

Alignment Scores:

Pred. No.: 2,75e-77 Length: 1400

Score: 84.00 Matches: 122

Percent Similarity: 98.39% Conservative: 0

Best Local Similarity: 98.39% Mismatches: 1

Query Match: 23.33% Indels: 2

DB: 10 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243

DB 257 TCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 316

QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263

DB 317 CTTTATCTCTGAGTCAGAACAGTGAAGGAGTGGCTAGTTCTTTCGAGAGAAATATC 376

QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283

DB 377 AACCCAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 436

QY 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303

DB 437 TCCATATACACGAAAGTAAAGCAAGACCATGAGGAAGTGTCTCTAGTAGCCAGTGAAGCA 496

QY 304 ValArgAlaIleAsp-LysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323

DB 497 GTTCGTGCTATTGA-GAAAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGA 555

QY 323 uThrLeuTyrLeuAlaProGlyGlyGlyAspTrrpIleTyrAspLeuGlyIleLysTyr 343

DB 556 AACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTATGATTGGGCATCAATA 615

QY 343 rSerPheThr 346

DB 616 TTCGTTTACA 625

RESULT 10

US-09-813-133A-3

; Sequence 3, Application US/09813133A

; Publication No. US20020137179A1

; GENERAL INFORMATION:

; APPLICANT: GAN, weiniu et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CL001173

; CURRENT APPLICATION NUMBER: US/09/813,133A

; CURRENT FILING DATE: 2001-08-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 55827

; TYPE: DNA

; ORGANISM: Human

US-09-813-133A-3

Alignment Scores:

Pred. No.: 4.15e-59 Length: 55827

Score: 68.00 Matches: 68

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 18.89% Indels: 0

DB: 9 Gaps: 0

US-09-980-881A-2 (1-360) x US-09-813-133A-3 (1-55827)

QY 229 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 248

DB 48643 GAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702

QY 249 GluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 268

DB 48703 GAACCAGAAAGTGAAGGAGTGGCTAGTTCTTTCGAGAGAAATATCAACCCAGATTAAAGCA 48762

QY 269 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 288

DB 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATATACACGAAGT 48822

QY 289 LysSerLysAspHisGluLeu 296

DB 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 11

US-10-212-877-3

; Sequence 3, Application US/10212877

; Publication No. US20030017574A1

```

; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Alignment Scores:
Pred. No.: 4,15e-59 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.89% Indels: 0
DB: 14 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-212-877-3 (1-55827)
QY 229 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 248
DB 48643 GAGGAGGTGATCCAGTCTCTCATGCTCGGAACTACTGTGGACTTATCTCTGAGTCA 48702
QY 249 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 268
DB 48703 GAACAGAGGTGAGGAGTGGCTAGTTCTTGAGAGAAATATCAACAGATTAAAGCA 48762
QY 269 TyrIleSerMetHisSerTyrSerClnHisIleValPheProTyrSerTyrThrArgSer 288
DB 48763 TACATCAGCATGTCATCTATCTCCAGCATATAGTGTTCATATCTCTATACACGAGT 48822
QY 289 LysSerLysAspHisGluGluLeu 296
DB 48823 AAAGCAAGACCATGAGGACTG 48846

RESULT 12
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

Alignment Scores:
Pred. No.: 2.1e-54 Length: 1272
Score: 62.00 Matches: 132
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 2
```

```

Query Match: 17.22% Indels: 4
DB: 15 Gaps: 0

US-09-980-881A-2 (1-360) x US-10-379-836-1 (1-1272)
QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
DB 1 ATGAAGCTTTTCAGCTCTTGAGTCTTGTACCCATTGTTCTTCTGTGAGCAGCATGTC 60
QY 21 PheAlaPheGlnSerGlyGlnValValLeuAlaLeuProArgThrSerArgGlnValGln 40
DB 61 TTGCGGTTTCAGAGTGCCAGGTTCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCAA 120
QY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuThrProValThrAlaAsp 60
DB 121 GTGCTACAGAAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCGGTAACAGCGGAC 180
QY 61 LeuIleVal-LysLysLysGlnValHisPhePheValAsnAla-SerAspValAspAsnV 80
DB 181 CTTATTGA-GAAGAAAAAACAAGTCCATTTTGTAAATTC-ATCTGATGTCGACAATG 238
QY 80 allysAlaHisLeuAsnValSerGlyIleProCysSerValLeuAlaAspValGluA 100
DB 239 TGAAGGCCATTTAAATGTGAGCGGAATTCATGCACTGCTCTGCTGGCAGATGTGGAAG 298
QY 100 spLeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrT 120
DB 299 ATCTTATTCAACAGCAGATTTTCCAACGACACAGTCAGCCCCCGAGCCTCGCATCTACT 358
QY 120 YrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 134
DB 359 ATGAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAA 402

RESULT 13
US-10-027-632-265133
; Sequence 265133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265133
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1547)
; OTHER INFORMATION: n = A, T, C or G
US-10-027-632-265133

Alignment Scores:
Pred. No.: 1.58e-34 Length: 1547
Score: 43.00 Matches: 43
```

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	11.94%	Indels:	0
DB:	13	Gaps:	0

US-09-980-881A-2 (1-360) x US-10-027-632-265133 (1-1547)

Qy	229	GluGluGlyAlaSerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer	248
Db	1417	GAGGAGGTGCATCCAGTCTCTCATGCTCGGAAACCTACTGTGGACTTATCTCTGAGTCA	1476

Qy	249	GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysala	268
Db	1477	GRAACGAAGTGAAGCGAGTGGCTAGTTTCTTCAGAGAATAATCAACACGATTAAAGCA	1536

Qy 269 TyrIleSer 271  
Db 1537 TACATCAGC 1545

RESULT 14

RESOLUTION 14  
US-10-027-632-265134  
; Sequence 265134, Application US/10027632  
; Publication No. US20020198371A1

Alignment Scores:	
Pred. No.:	1.58e-34
Score:	43.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	11.94%
DB:	13
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative:
	Matches: 43
	Length: 1547

US-09-980-881A-2 (1-360) x US-10-027-632-265134 (1-1547)

Qy	229	Gluc	Gluc	Ala	Ser	Ser	Ser	Cys	Ser	Glut	Thr	Tyr	Cys	Gly	Leu	Tyr	Pro	Glus	248
Nb	1417	GAG	GAG	GTC	GAT	CAG	TTC	TCT	ATG	CGG	ACC	TAT	GTG	CA	CTT	TAT	CTG	GAG	1476

Qy 249 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 268  
Df 1477 GlnCCGGCGCTGACGCCCGCAGTCCGTCTTCCTGCACGCAATATCATGACCGCGCTTTAAGCG 1550

Qy 269 TyrIleSer 271  
Db 1537 TACATCAGC 1545

RESULT 15

US-10-027-632-265135  
; Sequence 265135, Application US/10027632  
; Publication No. US20020198371A1

Alignment Scores:		
Pred. No.:	1.58e-34	1547
Score:	43.00	Matches: 43
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	11.94%	Indels: 0
DR:	13	Gaps: 0

US-09-980-881A-2 (1-360) x US-10-027-632-265135 (1-1547)

Qy 229 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 248  
1417 GGGGAGGTGGATCCAGTTCCTTCATGCTCGGAACTCTCTGTCGACTTATCTCGAGTCA 1476

**Qy**      249 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 268  
**pt**      1477 GNGGGNNCTNACCCGCGTGCCTTCCTTCGAGNCAGAAATATCATGCCAGATTAAAGA 1556

Qy 269 TyrIleSer 271

Search completed: October 27, 2004, 09:20:28  
Job time : 531.085 sec



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:06:11 ; Search time 18.6864 Seconds  
(without alignments)  
1277.637 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 1911  
Sequence: 1 MKCLSLAVLPIVFLCEQHV.....IKYFSTNPVPEKLLPLSLK 360

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 179518

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

ALIGNMENTS

RESULT 1  
US-09-309-317-5  
; Sequence 5, Application US/09309317  
; Patent No. 6277970  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Tremblay, Patrick  
; APPLICANT: Moore, Richard  
; APPLICANT: Westaway, David  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Lee, Inyoul  
; TITLE OF INVENTION: PrP-like Gene  
; FILE REFERENCE: 6510-130US1  
; CURRENT FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-09-309-317-5

Query Match 2.5%; Score 47; DB 3; Length 19;  
Best Local Similarity 33.3%; Pred. No. 2.4e+02;  
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 211 NHCIGTDLNSNFVSKHC 228  
||| : : : : :  
Db 1 NHCFGAEGNRYAANYC 18

RESULT 2  
US-09-541-345-44  
; Sequence 44, Application US/09541345  
; Patent No. 6774209  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC ANTIGEN (CEA)  
; FILE REFERENCE: Sequence Listing DIX-016.0 US  
; Patent No. 6774209  
; CURRENT APPLICATION NUMBER: US/09/541,345  
; CURRENT FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 44  
; LENGTH: 16  
; TYPE: PRT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	2.5	19	3	US-09-309-317-5 Sequence 5, Appl
2	42.5	2.2	16	4	US-09-541-345-44 Sequence 44, Appl
3	39.5	2.1	18	3	US-08-467-023-211 Sequence 211, App
4	39	2.0	13	2	US-08-596-387B-6 Sequence 6, Appl
5	39	2.0	13	3	US-09-067-615-6 Sequence 6, Appl
6	39	2.0	13	5	PCT-US95-09816A-6 Sequence 55, Appl
7	39	2.0	17	1	US-08-428-733A-55 Sequence 2, Appl
8	39	2.0	18	4	US-08-634-332A-2 Sequence 20, Appl
9	38.5	2.0	17	4	US-09-822-624-20 Sequence 198, App
10	38	2.0	14	2	US-08-585-589A-198 Sequence 47, Appl
11	38	2.0	16	4	US-09-340-620A-47 Sequence 140, App
12	38	2.0	17	2	US-08-685-589A-140 Sequence 25, Appl
13	38	2.0	17	4	US-08-182-967-25 Sequence 10, Appl
14	38	2.0	18	5	PCT-US93-03748-10 Sequence 59, Appl
15	38	2.0	19	1	US-08-382-013A-59 Sequence 71, Appl
16	38	2.0	19	1	US-08-382-013A-71 Sequence 25, Appl
17	38	2.0	19	4	US-08-817-832B-25 Sequence 7, Appl
18	37.5	2.0	14	4	US-09-671-089-7 Sequence 58, Appl
19	37.5	2.0	14	4	US-09-671-089-58 Sequence 66, Appl
20	37.5	2.0	17	4	US-09-440-781-66 Sequence 330, App
21	37	1.9	9	2	US-08-637-759B-330 Sequence 330, App
22	37	1.9	9	3	US-08-871-355A-330 Sequence 330, App
23	37	1.9	9	3	US-09-201-945-330 Sequence 9, Appl
24	37	1.9	12	3	US-08-293-728-9 Sequence 9, Appl
25	37	1.9	12	3	US-09-421-868-9 Sequence 1, Appl
26	37	1.9	14	2	US-08-634-001C-1 Sequence 15, Appl
27	37	1.9	14	3	US-09-470-618-15 Sequence 15, Appl

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CEA binding
; OTHER INFORMATION: polypeptide
US-09-541-345-44

Query Match          2.2%; Score 42.5; DB 4; Length 16;
Best Local Similarity 43.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 174 IWDCGHHAREWISPA 189
   ||||| : : ||
Db 1 IW-DCNLFKNQWFCEPA 15

RESULT 3
US-08-467-023-211
; Sequence 211, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;
; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D.;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,023
; FILING DATE: June 6, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,225
; FILING DATE: December 6, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: 025.6 US2D (IMI-028CPD2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-467-023-211

Query Match          2.1%; Score 39.5; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 166 KEOTAKNAIWID 177
   ||||| |||||
```

```
Db 2 KERTATN-IWID 12

RESULT 4
US-08-596-387B-6
; Sequence 6, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-596-387B-6

Query Match          2.0%; Score 39; DB 2; Length 13;
Best Local Similarity 58.3%; Pred. No. 9.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLIA 96
   ||||| |||
Db 1 NLCNIPCSALLS 12

RESULT 5
US-09-067-615-6
; Sequence 6, Application US/09067615
; Patent No. 6309645
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
```



NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/067,615  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/596,387  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-09-067-615-6

Query Match 2.0%; Score 39; DB 3; Length 13;  
Best Local Similarity 58.3%; Pred. No. 9.6e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96  
|: ||||| |:  
Db 1 NLCNIPCSALLS 12

RESULT 6  
PCT-US95-09816A-6  
Sequence 6, Application PC/TUS9509816A  
GENERAL INFORMATION:  
APPLICANT: Wong, Hing C.  
APPLICANT: Rhode, Peter R.  
APPLICANT: Widanz, Jon A.  
APPLICANT: Grammer, Susan  
APPLICANT: Edwards, Ana C.  
APPLICANT: Chavallaz, Pierre-Andre  
APPLICANT: Jiao, Jin-An  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 123  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/09816A  
FILING DATE: 31-JUL-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
PCT-US95-09816A-6

Query Match 2.0%; Score 39; DB 5; Length 13;  
Best Local Similarity 58.3%; Pred. No. 9.6e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96  
|: ||||| |:  
Db 1 NLCNIPCSALLS 12

RESULT 7  
US-08-428-733A-55  
Sequence 55, Application US/08428733A  
Patent No. 5763284  
GENERAL INFORMATION:  
APPLICANT: Tal, Rony  
APPLICANT: Wong, Hing C.  
APPLICANT: Casipit, Clayton  
APPLICANT: Chavallaz, Pierre-Andre  
APPLICANT: Wittman, Vaughan  
TITLE OF INVENTION: Methods for Peptide Synthesis and  
Purification  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DADE INTERNATIONAL, INC.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: US  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,733A  
FILING DATE: 04-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,178  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: DA-4623 CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-428-733A-55

Query Match 2.0%; Score 39; DB 1; Length 17;  
Best Local Similarity 58.3%; Pred. No. 1.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
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Db 5 NLCNIPCSALLS 16

RESULT 8  
US-08-634-332A-2  
Sequence 2, Application US/08634332A  
Patent No. 6531578  
GENERAL INFORMATION:  
APPLICANT: ROBERT WEBBER  
TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL ANTIBODY REACTIVE TO HUMAN INOS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LAMPE  
STREET: 1990 N CALIFORNIA BOULEVARD, SUITE 720  
CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,332A  
FILING DATE: 12-Apr-1996  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE  
ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 12280  
TELEPHONE: (925) 937-1515  
TELEFAX: (925) 937-1529  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
NAME/KEY: MOUSE INOS (25-42)  
LOCATION:  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-634-332A-2

Query Match 2.0%; Score 39; DB 4; Length 18;  
Best Local Similarity 43.8%; Pred. No. 1.6e+03;  
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Qy 85 NVSGIPCSVLLADVED 100  
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Db 3 NVKTKPCAVLSPTIQD 18

RESULT 9  
US-09-822-624-20  
Sequence 20, Application US/09822624  
Patent No. 6440714  
GENERAL INFORMATION:  
APPLICANT: Abell, Creed W.  
APPLICANT: Kwan, Sua-Wah  
APPLICANT: Zhou, Binhua  
APPLICANT: Wo, Bo  
TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B  
FILE REFERENCE: D6237PCT  
CURRENT APPLICATION NUMBER: US/09/822,624  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 2000-03-30  
PRIOR FILING DATE: US 60/193,178  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 20  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence flanking the covalent FAD  
OTHER INFORMATION: binding residue of human monooxidase B (MAO B)  
US-09-822-624-20

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Best Local Similarity 53.3%; Pred. No. 1.7e+03;  
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Db 1 WCEE-QYSGGCTTY 14

RESULT 10  
US-08-685-589A-198  
Sequence 198, Application US/08685589A  
Patent No. 5916872  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Leo  
APPLICANT: Chen, Jie  
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD  
NUMBER OF SEQUENCES: 222  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,589A  
FILING DATE: 24-JUL-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-026-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090

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; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 198:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /product= "Cyclic"
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; US-08-685-589A-198
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; Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; QY 237 CSETYCGLYP 246
; DB 3 CSRRYCVCP 12
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; RESULT 11
; US-09-340-620A-47
; Sequence 47, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
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; US-09-340-620A-47
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; Query Match 2.0%; Score 38; DB 4; Length 16;
; Best Local Similarity 52.6%; Pred. No. 1.7e+03;
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; DB 1 YC--YPERDPE--EVFAFL 15
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; RESULT 12
; US-08-685-589A-140
; Sequence 140, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
;
; US-09-980-881a-2.std.ra1
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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION: /product= "Cyclic"
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; US-08-685-589A-140
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; Query Match 2.0%; Score 38; DB 2; Length 17;
; Best Local Similarity 41.2%; Pred. No. 1.9e+03;
; Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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; QY 178 CGIHAREWISPAFLWLF 194
; DB 1 CLRYCRRRCVRFCLWF 17
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; RESULT 13
; US-08-182-967-25
; Sequence 25, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/462,471  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,867  
FILING DATE: 14-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/644,611  
FILING DATE: 22-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/530,229  
FILING DATE: 30-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/382,085  
FILING DATE: 18-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/382,086  
FILING DATE: 18-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/326,314  
FILING DATE: 21-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IM 9830  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-182-967-25

Query Match 2.0%; Score 38; DB 4; Length 17;  
Best Local Similarity 42.9%; Pred. No. 1.9e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 110 TVSPRASASYEQY 123  
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Db 4 SINTRASGRHYEQF 17

RESULT 14  
PCT-US93-03748-10  
Sequence 10, Application PC/TUS9303748  
GENERAL INFORMATION:  
APPLICANT: Howard, Russell J.  
APPLICANT: Leung, Lawrence L.K.  
TITLE OF INVENTION: Modulation of Thrombospondin-CD36 Interactions  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: One Giralda Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 4.00B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03748  
FILING DATE: 19930428  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/876,287  
FILING DATE: 30-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dulak, Norman C.

REGISTRATION NUMBER: 31,608  
REFERENCE/DOCKET NUMBER: DX0270K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-822-7375  
TELEFAX: 201-822-7039  
TELEX: 219165  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-03748-10

Query Match 2.0%; Score 38; DB 5; Length 18;  
Best Local Similarity 43.8%; Pred. No. 2.1e+03;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 34 RTSRQVOVLNLTYY 49  
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Db 3 KPSEKIQLNLRNY 18

RESULT 15  
US-08-382-013A-59  
Sequence 59, Application US/08382013A  
Patent No. 5631222  
GENERAL INFORMATION:  
APPLICANT: Shibata, Kenji  
APPLICANT: Suzawa, Toshiyuki  
APPLICANT: Yamasaki, Motoo  
APPLICANT: Tanaka, Takeo  
APPLICANT: Tsukuda, Ei-ji  
APPLICANT: Yamada, Ko-ji  
APPLICANT: Ohno, Tetsuji  
TITLE OF INVENTION: Endothelin-Antagonizing Peptide  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/382,013A  
FILING DATE: 10-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 155031/93  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lippert, Neil T.  
REGISTRATION NUMBER: 25888  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8200  
TELEFAX: 212-354-8113  
TELEX: 233188  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-382-013A-59

Query Match 2.0%; Score 38; DB 1; Length 19;

Best Local Similarity 62.5%; Pred. No. 2.3e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 4 GWGNDWY 11

Search completed: October 27, 2004, 01:31:42  
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GenCore version 5.1.6  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1364641 seqs, 323758627 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	48	2.5	11	16 US-10-343-509-10	Sequence 10, Appl
2	47	2.5	19	9 US-09-799-760-5	Sequence 5, Appl
3	46	2.4	11	15 US-10-410-764-87	Sequence 87, Appl
4	42.5	2.2	16	10 US-09-825-517A-44	Sequence 44, Appl
5	41	2.1	13	15 US-10-469-304-55	Sequence 55, Appl
6	41	2.1	18	16 US-10-742-379-90	Sequence 90, Appl
7	40	2.1	14	15 US-10-436-715-431	Sequence 431, Appl
8	39	2.0	13	9 US-09-848-164-6	Sequence 6, Appl
9	39	2.0	13	9 US-09-957-674-5	Sequence 5, Appl
10	39	2.0	13	9 US-09-900-379-6	Sequence 6, Appl
11	38.5	2.0	17	9 US-09-822-624-20	Sequence 20, Appl
12	38	2.0	13	14 US-10-126-845-91	Sequence 91, Appl
13	38	2.0	16	9 US-09-728-721-47	Sequence 47, Appl

14	38	2.0	16	14	US-10-295-981-47	Sequence 47, Appl
15	38	2.0	18	14	US-10-125-869A-23	Sequence 23, Appl
16	38	2.0	18	15	US-10-462-262-247	Sequence 247, Appl
17	38	2.0	18	16	US-10-364-645A-54	Sequence 54, Appl
18	38	2.0	19	8	US-08-817-832B-25	Sequence 25, Appl
19	38	2.0	19	15	US-10-440-435-25	Sequence 25, Appl
20	37.5	2.0	14	14	US-10-126-845-7	Sequence 7, Appl
21	37.5	2.0	14	14	US-10-126-845-65	Sequence 65, Appl
22	37.5	2.0	14	14	US-10-116-275-95	Sequence 95, Appl
23	37.5	2.0	14	16	US-10-764-235-7	Sequence 7, Appl
24	37.5	2.0	14	16	US-10-764-235-58	Sequence 58, Appl
25	37.5	2.0	14	16	US-10-034-374-32	Sequence 32, Appl
26	37.5	2.0	17	15	US-10-624-153-66	Sequence 66, Appl
27	37.5	2.0	18	16	US-10-712-447-22	Sequence 22, Appl
28	37	1.9	13	15	US-10-469-304-56	Sequence 56, Appl
29	37	1.9	14	9	US-09-740-211-15	Sequence 15, Appl
30	37	1.9	14	13	US-10-007-968-15	Sequence 15, Appl
31	37	1.9	14	14	US-10-233-400-15	Sequence 15, Appl
32	37	1.9	15	14	US-10-371-540-30	Sequence 30, Appl
33	37	1.9	15	16	US-10-327-598-74	Sequence 74, Appl
34	37	1.9	16	14	US-10-225-567A-1864	Sequence 1864, Appl
35	37	1.9	16	14	US-10-083-768-15	Sequence 15, Appl
36	37	1.9	16	15	US-10-609-217-75	Sequence 75, Appl
37	37	1.9	16	15	US-10-632-388-75	Sequence 75, Appl
38	37	1.9	16	15	US-10-651-723-75	Sequence 75, Appl
39	37	1.9	16	15	US-10-645-761-75	Sequence 75, Appl
40	37	1.9	16	15	US-10-666-696-75	Sequence 75, Appl
41	37	1.9	16	15	US-10-653-048-75	Sequence 75, Appl
42	37	1.9	18	14	US-10-105-232-194	Sequence 194, Appl
43	37	1.9	18	14	US-10-189-437-181	Sequence 181, Appl
44	37	1.9	19	9	US-09-864-761-41546	Sequence 41546, Appl
45	37	1.9	19	10	US-09-931-325A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-10-343-509-10  
; Sequence 10, Application US/10343509  
; Publication No. US20040101865A1  
; GENERAL INFORMATION:  
; APPLICANT: BASF  
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof  
; FILE REFERENCE: 0050/51654  
; CURRENT APPLICATION NUMBER: US/10/343,509  
; CURRENT FILING DATE: 2003-01-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
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; LENGTH: 11  
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; ORGANISM: Euglena gracilis  
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; NAME/KEY: VARIANT  
; LOCATION: (11)  
; OTHER INFORMATION: Xaa = (Phe/Tyr)  
US-10-343-509-10

Query Match 2.5%; Score 48; DB 16; Length 11;  
Best Local Similarity 70.0%; Pred. No. 5.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 331 GGGDWIYDLG 340  
Db 1 GGGDWAYDIG 10

RESULT 2  
US-09-799-760-5  
; Sequence 5, Application US/09799760  
; Patent No. US20010021771A1  
; GENERAL INFORMATION:

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; APPLICANT: Prusiner, Stanley
; APPLICANT: Tremblay, Patrick
; APPLICANT: Moore, Richard
; APPLICANT: Westaway, David
; APPLICANT: Hood, Leroy E.
; APPLICANT: Lee, Inyoul
; TITLE OF INVENTION: PrP-like Gene
; FILE REFERENCE: 6510-130CON
; CURRENT APPLICATION NUMBER: US/09/799,760
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/309,317
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide
US-09-799-760-5

Query Match      2.5%; Score 47; DB 9; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      211 NHCIGTDLNPNFVSKHC 228
Db      1 NHCFGAGNRYVYAANYC 18
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RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0520NM1M
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match      2.4%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 8.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      273 HSYSQHIVFPY 283
Db      1 HSYSQMLMPY 11
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RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421, 1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match      2.2%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred. No. 3.4e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy      174 IWIDCGIHAREWISPA 189
Db      1 IW-DCNLFKNQWFCFA 15
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RESULT 5
US-10-469-304-55
; Sequence 55, Application US/10469304
; Publication No. US200400091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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US-10-469-304-55

Query Match 2.1%; Score 41; DB 15; Length 13;  
Best Local Similarity 42.1%; Pred. No. 3.5e+03;  
Matches 8; Conservative 2; Mismatches 1; Indels 1;

QY 53 LMQPVTADLVKKQVHFF 71  
||| |  
Db 2 LMQP-----KRECHFF 12

RESULT 6

US-10-742-379-90

Sequence 90, Application US/10742379

Publication No. US20040181033A1

GENERAL INFORMATION:

APPLICANT: Han, HQ

APPLICANT: Min, Hongsung

APPLICANT: Boone, Thomas Charles

TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN

FILE REFERENCE: A-828 (US)

CURRENT APPLICATION NUMBER: US/10/742,379

CURRENT FILING DATE: 2003-12-19

PRIOR APPLICATION NUMBER: US 60/435,923

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 634

SOFTWARE: PatentIn version 3.2

SEQ ID NO 90

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Myostatin Binding Peptide

US-10-742-379-90

Query Match 2.1%; Score 41; DB 16; Length 18;  
Best Local Similarity 83.3%; Pred. No. 5.6e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 226 HWCEEG 231  
||| |  
Db 2 HWCEQG 7

RESULT 7

US-10-436-715-431

Sequence 431, Application US/10436715

Publication No. US20040018976A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,

TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF

FILE REFERENCE: D0262 NP

CURRENT APPLICATION NUMBER: US/10/436,715

CURRENT FILING DATE: 2003-05-13

PRIOR APPLICATION NUMBER: U.S. 60/380,336

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 471

SOFTWARE: PatentIn version 3.2

SEQ ID NO 431

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

US-10-436-715-431

Query Match 2.1%; Score 40; DB 15; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.9e+03;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 44 NLTTTYBIVLWQ 55  
:|:|:|:|:  
Db 3 DLNTGYDVLWK 14

RESULT 8

US-09-848-164-6

Sequence 6, Application US/09848164

Patent No. US20020034513A1

GENERAL INFORMATION:

APPLICANT: Rhode, Peter R.

Jiao, Jin-An

Burkhardt, Martin

Wong, Hing

TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dade International, Inc.

STREET: 1717 Deerfield Road

CITY: Deerfield

STATE: Illinois

COUNTRY: USA

ZIP: 60015

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/848,164

FILING DATE: 03-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/067,615

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/382,454

FILING DATE: 01-FEB-1995

APPLICATION NUMBER: US 08/283,302

FILING DATE: 29-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Pearson, Louise S.

REGISTRATION NUMBER: 32,369

REFERENCE/DOCKET NUMBER: STR-4665-CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 267-5300

TELEFAX: (708) 267-5376

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-848-164-6

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 85 NVSGIPCSVLLA 96  
|:|:|:|:|:  
Db 1 NLCNIPCSALLS 12

RESULT 9

US-09-957-674-5

Sequence 5, Application US/09957674

Patent No. US20020120948A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: Methods for Expressing Gene Products

FILE REFERENCE: 18396/2072

CURRENT APPLICATION NUMBER: US/09/957,674

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: GB990736

PRIOR FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: PCT/GB00/01225

;; PRIOR FILING DATE: 2000-03-30  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: Patent in version 3.1  
;; SEQ ID NO 5  
;; LENGTH: 13  
;; TYPE: PRT  
;; ORGANISM: Chicken  
US-09-957-674-5

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
|: |||||  
Db 1 NLCNIPCSALLS 12

RESULT 10  
US-09-900-379-6  
; Sequence 6, Application US/09900379  
; Publication No. US20020198144A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; Rhoads, Peter R.  
; Widanz, Jon A.  
; Grammer, Susan  
; Edwards, Ana C.  
; Chavallaz, Pierre-Andre  
; Jiao, Jin-An  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 123  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/900,379  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,084  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/US95/09816  
; FILING DATE: 31-JUL-1995  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995  
; APPLICATION NUMBER: US 08/283,302  
; FILING DATE: 29-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pearson, Louise S.  
; REGISTRATION NUMBER: 32,369  
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 267-5300  
; TELEFAX: (708) 267-5376  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-900-379-6

Query Match 2.0%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.5e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 85 NVSGIPCSVLLA 96  
|: |||||  
Db 1 NLCNIPCSALLS 12

RESULT 11  
US-09-822-624-20  
; Sequence 20, Application US/09822624  
; Publication No. US20020004233A1  
; GENERAL INFORMATION:  
; APPLICANT: Abell, Creed W.  
; APPLICANT: Kwan, Sua-Wah  
; APPLICANT: Zhou, Binhua  
; APPLICANT: Wo, Bo  
; TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B  
; FILE REFERENCE: D6237PCT  
; CURRENT APPLICATION NUMBER: US/09/822,624  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 2000-03-30  
; PRIOR FILING DATE: US 60/193,178  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence flanking the covalent FAD  
; OTHER INFORMATION: Binding residue of human monooxidase B (MAO B)  
US-09-822-624-20

Query Match 2.0%; Score 38.5; DB 9; Length 17;  
Best Local Similarity 53.3%; Pred. No. 9.1e+03;  
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 227 WCEGASSSSGCSEY 241  
|: |||||  
Db 1 WCEG-QVSGGCYTTY 14

RESULT 12  
US-10-126-845-91  
; Sequence 91, Application US/10126845  
; Publication No. US20030181367A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Lambkin, Imelda J.  
; APPLICANT: Pinilla, Clemencia  
; APPLICANT: Houghten, Richard  
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM  
; FILE REFERENCE: E1067/20058  
; CURRENT APPLICATION NUMBER: US/10/126,845  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 91  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: D form peptide  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(13)  
; OTHER INFORMATION: D form retroinversion peptide  
US-10-126-845-91

Query Match 2.0%; Score 38; DB 14; Length 13;  
Best Local Similarity 46.2%; Pred. No. 6.9e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 CSLAVLVPIVLC 16  
| :|||::: |  
Db 1 CPAALLVPLLVAC 13

RESULT 13  
US-09-728-721-47  
; Sequence 47, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-47

Query Match 2.0%; Score 38; DB 9; Length 16;  
Best Local Similarity 52.6%; Pred. No. 9.3e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

QY 241 YCGLYPESEPEVKAVASEFL 259  
| | | | | : | | | | |  
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 14  
US-10-295-981-47  
; Sequence 47, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-981-47

Query Match 2.0%; Score 38; DB 14; Length 16;  
Best Local Similarity 52.6%; Pred. No. 9.3e+03;  
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

QY 241 YCGLYPESEPEVKAVASEFL 259  
| | | | | : | | | | |  
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 15  
US-10-125-869A-23  
; Sequence 23, Application US/10125869A  
; Publication No. US20030199671A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac Jesus  
; APPLICANT: Wu, Qi-Long  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Stochl, Mark  
; APPLICANT: Ranschoff, Thomas C.  
; APPLICANT: Potter, M. Daniel (deceased)  
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION  
; TITLE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 3421.1006-001  
; CURRENT APPLICATION NUMBER: US/10/125,869A  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/284,534  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc region binding polypeptide  
US-10-125-869A-23

Query Match 2.0%; Score 38; DB 14; Length 18;  
Best Local Similarity 35.0%; Pred. No. 1.1e+04;  
Matches 7; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 178 CGIHAREWISPAFCLWFIGH 197  
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Db 1 CRACSRDW--FGALVWCAGH 18

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Job time : 46.3814 secs



GenCore version 5.1.6  
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(without alignments)  
2705.583 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 1911  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=std.rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*\*

- 1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:\*\*
- 2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:\*\*
- 3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:\*\*
- 4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:\*\*
- 5: /cgn2.6/ptodata/1/ina/PCTUS.COMB.seq:\*\*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1849.5	96.8	1625	4	US-09-813-133A-1
2	1832	95.9	1272	2	US-08-869-057-1
3	1832	95.9	1749	1	US-07-649-591B-2
4	1832	95.9	1749	1	US-08-277-540-2
5	1832	95.9	1749	1	US-08-430-787A-2
6	640.5	33.5	1215	1	US-08-696-139-1
7	639	33.4	1263	2	US-08-860-882A-56
8	639	33.4	1263	4	US-09-011-769A-38
9	631.5	33.0	1284	2	US-08-860-882A-71
10	631.5	33.0	1284	4	US-09-011-769A-55
11	623	32.6	2154	3	US-09-171-945-124
12	619.5	32.4	1622	4	US-09-023-655-1020
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					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 56, Appl
					Sequence 38, Appl
					Sequence 71, Appl
					Sequence 55, Appl
					Sequence 124, App
					Sequence 1020, Ap

13	611.5	32.0	1311	4	US-09-675-305-9
14	611.5	32.0	1311	4	US-10-200-344-9
15	604	31.6	927	2	US-08-782-760-5
16	604	31.6	927	5	PCT-US96-00995-5
17	576	30.1	921	1	US-08-696-139-3
18	564	29.5	2128	4	US-09-675-305-13
19	564	29.5	2128	4	US-10-200-344-13
20	561	29.4	999	2	US-08-860-882A-67
21	561	29.4	999	4	US-09-011-769A-50
22	561	29.4	1053	2	US-08-860-882A-64
23	561	29.4	1053	4	US-09-011-769A-46
24	554	29.0	1053	4	US-09-463-451-27
25	554	29.0	1053	4	US-09-463-451-28
26	554	29.0	1059	2	US-08-860-882A-74
27	554	29.0	1059	4	US-09-011-769A-59
28	553	28.9	1059	2	US-08-860-882A-77
29	553	28.9	1059	4	US-09-011-769A-63
30	546	28.6	1200	4	US-09-710-099-7
31	546	28.6	1200	4	US-10-200-910-7
32	543	28.4	1870	3	US-09-171-945-112
33	528.5	27.7	1050	4	US-09-675-305-11
34	528.5	27.7	1050	4	US-10-200-344-11
35	519.5	27.2	1311	4	US-09-710-099-5
36	519.5	27.2	1311	4	US-10-200-910-5
37	513	26.8	1251	3	US-08-640-906-3
38	513	26.8	1251	3	US-09-395-936-3
39	487.5	25.5	1257	3	US-08-640-906-1
40	487.5	25.5	1257	3	US-09-395-936-1
41	460.5	24.1	945	4	US-09-710-099-3
42	460.5	24.1	945	4	US-09-710-099-11
43	460.5	24.1	945	4	US-10-200-910-3
44	460.5	24.1	945	4	US-10-200-910-11
45	458.5	24.0	2247	4	US-09-710-099-15

ALIGNMENTS

RESULT 1

US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weinlu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 6.66e-227 Length: 1625  
Score: 1849.50 Matches: 355  
Percent Similarity: 94.18% Conservative: 1  
Best Local Similarity: 93.92% Mismatches: 4  
Query Match: 96.78% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

QY	1	MetLyeLeuCyseSerLeuAlaValLeuValProileValLeuPheCysGluGlnHisVal	20
DB	17	ATGAGCTTTTGAGCTTCCTTGACCTCTTGACCATTTCTTCTTGTGAGCAGCATGTC	76
QY	21	PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln	40

Db 77 TTCGGTTTCAGAGTGGCAAGTTCTAGCTGCTCTTCTCTAGAACCTCTAGCAAGTTCAA 136  
 Qy 41 ValLeuGlnAenLeuThrThrTyrGluLeuValLeuThrGlnProValThrAlaAsp 60  
 Db 137 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGAC 196  
 Qy 61 LeuLeuValLysLysGlnValHisPhePheValAenAlaSerAspValAsnVal 80  
 Db 197 CTTATTGTGAAGAAAAAACAAGTCATTTTTTGTAAATGATCTGTGTCGACAAATGTG 256  
 Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
 Db 257 AAAGCCATTTAAATGTAGGGGAATTCATGTCAGTGTCTTCTGGCAGATGTGAAGAT 316  
 Qy 101 LeuLeuGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
 Db 317 CTTATTCAACAGCAGATTTCACACACACAGTCAGCCCGCAGCGCTCCGCTACTAT 376  
 Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
 Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCAT 436  
 Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
 Db 437 CTTGATATGCTTACAAAAATCCACATTCGATCCTCATTTGAGAAGTACCCACTCTATGTT 496  
 Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIle 180  
 Db 497 TTAAGGTTTCTGGAAGAAAGAACAGCAGCAAAAAATGCCATATGATGATGCTGGAATC 556  
 Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200  
 Db 557 CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATAAATCGAATG 616  
 Qy 201 TrpArgLysAsnArgSerPheTyrAlaAenAenHisCysIleGlyThrAspLeuAsnSer 220  
 Db 617 TGGAGAAAGAACCGTTCTTCTATGCGAACCAATCATTCGATCGGACAGACCTGATAGG 676  
 Qy 221 AenPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
 Db 677 AACTTTGCTTCAAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGAAACC 736  
 Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
 Db 737 TACTGTGACTTTATCTGAGTCAAGAACAGAGTGAAGCGAGTGGCTAGTTTCTTGAGA 796  
 Qy 261 ArgAenIleAenGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280  
 Db 797 AGAATATACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 856  
 Qy 281 PheProTyrSerTyrThrArgSerLysLysAspHisGluLeuSerLeuValAla 300  
 Db 857 TTTCCATATCTCATACAGAAATAAAGCAAGAACCAACCATGAGGAACCTGCTCTAGTAGCC 916  
 Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAenThrArgTyrThrHisGlyHis 320  
 Db 917 AGTGAAGCAGTTCGTGCTATTGAGAAATATAGTAAAAATACAGGTATACATGCGCCAT 976  
 Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyrAspLeuGly 340  
 Db 977 GGCTCAGAAACCTTATACCTAGTCTCTGGAGTGGGACGATTGGATCTATGATTTGGGC 1036  
 Qy 341 IleLysTyrSerPhe----- 345  
 Db 1037 ATCAATATTCGTTTACAATTAACCTTCGAGATACGGGCACATACGGATTCTTGTGTCGC 1096  
 Qy 346 -----ThrSerAenProValGluLysLeuLeuProLeuSerLeuLys 360  
 Db 1097 GAGCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGGTGTCTCTAAAA 1148

RESULT 2

US-08-869-057-1

; Sequence 1, Application US/08869057

; Patent No. 5985562  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morser, Michael J  
 ; APPLICANT: Nagashima, Mariko  
 ; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
 ; TITLE OF INVENTION: Risk  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Berlex Biosciences Legal Department  
 ; STREET: 15049 San Pablo Avenue  
 ; CITY: Richmond  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94804-0099  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/08/869,057  
 ; APPLICATION NUMBER: US/08/869,057  
 ; FILING DATE: 03-JUN-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Washlien, Wendy L  
 ; REGISTRATION NUMBER: 36,301  
 ; REFERENCE/DOCKET NUMBER: 51509AUSM1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 510-262-5411  
 ; TELEFAX: 510-262-7095  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1272 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Eaton, Dan L.  
 ; AUTHORS: Malloy, Beth E.  
 ; AUTHORS: Tsai, Siao P  
 ; AUTHORS: Henzel, William  
 ; AUTHORS: Drayna, Dennis  
 ; TITLE: Isolation, Molecular Cloning, and Partial  
 ; TITLE: Characterization of a No. 5985562zel Carboxypeptidase B  
 ; JOURNAL: J. Biol. Chem.  
 ; VOLUME: 266  
 ; ISSUE: 32  
 ; PAGES: 21833-21838  
 ; DATE: No. 5985562 15-1991  
 ; US-08-869-057-1  
 ;  
 ; Alignment Scores:  
 ; Pred. No.: 7,696-225 Length: 1272  
 ; Score: 1832.00 Matches: 357  
 ; Percent Similarity: 86.27% Conservative: 1  
 ; Best Local Similarity: 86.02% Mismatches: 2  
 ; Query Match: 95.87% Indels: 55  
 ; DB: 2 Gaps: 2  
 ;  
 ; US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)  
 ;  
 ; Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
 ; Db 1 ATGAAGCTTTGCAGCTCCTTGTAGTCCCTTGTCTCTGTGAGCAGCATGTC 60  
 ; Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
 ; Db 61 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAA 120  
 ; Qy 41 ValLeuGlnAenLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60

Db 121 GTTCTACAGAACTTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGAC 180  
Qy 61 LeuileValLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80  
Db 181 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTGTAAATGTCATCTGATGTGACAAATGTG 240  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 241 AAAGCCCATTTAAATGTAGCGGAATTCATGCACTGCTTGTCTGGCAGAGCTGGAAGAT 300  
Qy 101 LeuileGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 301 CTTATTCAACAGCAGATTTCACACAGACAGTCAGCCCGAGCCCTCGCATCGTACTAT 360  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHis 140  
Db 361 GAACAGATATCACTCAATAAGAAATCTATTCTGGATAGAAATTTATACTGAGAGGAT 420  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 421 CCGTATATGCTTACAAAATCCACATTTGGATCTCTCATTTGAGAAGTACCCACTCTATGT 480  
Qy 161 LeuLysValSerGlyLysGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIle 180  
Db 481 TTAAGGTTTCTGGAAGAAAGAACAAACAGCCAAAATGCCATATGATTCAGCTGTGGAATC 540  
Qy 181 HisAlaArgGluTyrIleSerProAlaPheCysLeuTyrPheIleGlyHis 197  
Db 541 CATGCCAGAAATGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATACTCAA 600  
Qy 197 ----- 197  
Db 601 TTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATG 660  
Qy 198 -----AsnArgMetTyrArgLys 203  
Db 661 CCGGTGGTTAATGTGACGGTTATGACTACTCATGCAAGAAAGATCGAATGTGGAGAAAG 720  
Qy 204 AsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223  
Db 721 AACCGTTCTTCTATCGAACAATCATTTGCATCGGAACAGACCTGAAATAGGAACCTTTGCT 780  
Qy 224 SerLysHisTyrCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243  
Db 781 TCAAAACACTGGTGTGAGGAAGTGCATTCAGTTCTCTCATGCTCGGAACCTACTGTGA 840  
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAnile 263  
Db 841 CTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTTCTTGAGAGAAATATC 900  
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283  
Db 901 AACCAATTAAGCATACATACAGCATGCATTCATCTCCAGCATATAGTGTTCATAT 960  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303  
Db 961 TCTATACAGAAAGTAAAGCAAGAACCATGAGAACTGTCTCTAGTAGCCAGTGAAGCA 1020  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1021 GTTCGTGCTATTGAGAAACACTAGTAAATAATACAGGTATATACATGGCCATGGCTCAGAA 1080  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyr 343  
Db 1081 ACCTTATACCTAGTCTCTGAGGTGGGAGCATTTGGATCTATGATTGGGCATCAATAT 1140  
Qy 344 SerPhe-----Th 346  
Db 1141 TCGTTTTCATAAATGAACTTCGAGATACGGGCACATACGGATTTCTGTGCGGAGCGTTAC 1200  
Qy 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1201 ATCAACCCACCTGTAGAGAAAGCTTTTGGCGCTGTCTCTAAA 1243

RESULT 3  
US-07-649-591B-2  
Sequence 2, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161e1 Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: hybridization probe  
LOCATION: 133 to 178  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: potential clip site  
LOCATION: 380 to 382  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 41 to 106  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-649-591B-2  
Alignment Scores:  
Pred. No.: 1.34e-224 Length: 1749  
Score: 1832.00 Matches: 357  
Percent Similarity: 86.27% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-2 (1-360) x US-07-649-591B-2 (1-1749)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGCAGCGCTTGCAGTCTTGACCACTGTTCTTCTGTGAGCAGCATGTC 100

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Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db |||||
101 TTCGGTTTCAGAGTGGCAAGTTCTAGCTCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160
Qy 41 ValLeuGlnAenLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db |||||
161 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 220
Qy 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Db |||||
221 CTTATTGTGAAGAAAAACAAGTCCATTTTTTGTAAATGCATCTGATGTCGACAAATGTG 280
Qy 81 LysAlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db |||||
281 AAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTGCTGGCAGAGCTGGAAGAT 340
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db |||||
341 CTTATTTCACAGCAGATTTCACAGACACATGTCAGCCCCCGAGCTCCGCATCGTACTAT 400
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db |||||
401 GAACAGTATCACTCACTAAATGAAATCTATTCTTGGATAGAATTTATAACTGAGAGCAT 460
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db |||||
461 CCTGATATGCTTACAAAAATCCATTTGGATGCTCCTCATTTGAGAAAGTACCCACTCTATGTT 520
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db |||||
521 TTAAGGTTTCTGANAAGAACAAACACGCCAAAATGCCATATGGATTGACTGTGGATC 580
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db |||||
581 CATGCCAGAAATGGATCTCTCTGCTTCTCTGTTCTGTTGTTTCATAGGCCATATAACTCAA 640
Qy 197 ----- 197
Db |||||
641 TTCTATGGGATAATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATG 700
Qy 198 -----AsnArgMetTrpArgLys 203
Db |||||
701 CCGGTGTTTATGTGGAGGTTATGACTACTCATCGGAAAAGAAATCGAATGTGGAGAAAG 760
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAenSerAsnPheVal 223
Db |||||
761 AACCGTTCTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTGCT 820
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243
Db |||||
821 TCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAAACCTACTGTGGA 880
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaLaserPheLeuArgAsnIle 263
Db |||||
881 CTTTATCTCTAGTCAGAACCAAGAGAGTGAAGCAGTGGCTAGTTCTTGAGAGAAATATC 940
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
Db |||||
941 AACAGATTAAGCATATACATCAGCATGCTATCTACTCCAGCATATAGTGTTCCTATAT 1000
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla 303
Db |||||
1001 TCCTATACCAAGATTAAGCAAGAACCATCAGGAACCTGCTCTAGTAGCCAGTGAAGCA 1060
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
Db |||||
1061 GTTGTGCTATTGAGAAAACCTAGTAAANATACAGGATATACATAGCCCTGCTCAGAA 1120
Qy 324 ThrLeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLysTyr 343
Db |||||
1121 ACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCATCAAAATAT 1180
Qy 344 SerPhe-----Th 346
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Db 1181 TCGTTTACAATTGAATTCGAGATACGGGCACATACGAGATTCTTGTCGGGACGTTAC 1240
Qy 346 rSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360
Db |||||
1241 ATCAAAACCCACTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1283

RESULT 4
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Baton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Alignment Scores:
Pred. No.: 1.34e-224 Length: 1749
Score: 1832.00 Matches: 357
Percent Similarity: 86.27% Conservative: 1
Best Local Similarity: 86.02% Mismatches: 2
Query Match: 95.87% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db |||||
41 ATGAAGCTTTTGCAGCCTTGACGCTTGACGCTCTTGATCCCATTTGTTCTCTGTGAGACGATGTC 100
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLaserProArgThrSerArgGlnValGln 40
Db |||||
101 TTCGGTTTCAGAGTGGCAAGTTCTAGCTCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160
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Qy 346 rSerAsnProValGluLysLeuProLeuSerLeuLys 360  
Db 1241 ATCAACCCACCTGTAGAGAGCTTTTGGCGCTGTCTCTAAA 1283

RESULT 5  
US-08-430-787A-2  
; Sequence 2, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-430-787A-2

Alignment Scores:  
Pred..No.: 1,34e-224 Length: 1749  
Score: 1032.00 Matches: 357  
Percent Similarity: 86.2% Conservative: 1  
Best Local Similarity: 86.02% Mismatches: 2  
Query Match: 95.87% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-2 (1-360) x US-08-430-787A-2 (1-1749)

Qy 1 MetLysLeuCySerSerLeuAlaValProIleValLeuPheCysGluGlnHisVal 20  
Db 41 ATGAAGCTTTGAGCCTTCAGCTTCCTGTACCATTTGTTCTCTGTGAGCAGCATGTC 100

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40  
Db 101 TTGCGCTTTTTCAGAGTGGCCAAAGTCTTAGCTCTCTTAGAACCTCTTAGGCAGATTCAA 160





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Qy 105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db 304 CAGTTTGTATGACCGGGTT-----CGTCAACAGGACACACAGTTATGAGAAGTACAAAC 354
Qy 125 SerLeuAsnGluIleTyrSerTyrIleGluPheIleThrGluArgHisProAspMetLeu 144
Db 355 AAGTGGGAAACGATAGAGCTTGGACTCAACAGTCGCCATGAGATCCAGCCCTCATC 414
Qy 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValser 164
Db 415 TCTCGCAGTGTATCGGAACACATTTGAGGACGCGCTATTACCTCTGAAGTT--- 471
Qy 165 GlyLysGluGlnThrAlaLysAsnNlaIleTrpIleAspCysGlyIleHisAlaArgGlu 184
Db 472 GCGAAAGCTGGCAAAATAAGCCTGCCATTTTCATGGAGCTGTGGTTTCCATGCCAGAGAG 531
Qy 185 TrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 532 TGGATTCTCTGCAATTCCTGCAGTGGTTTGTAGAGAGGCTGTTCGTACCTATGGACGT 591
Qy 195 ----- 195
Db 592 GAGATCCAAAGTCACAGAGCTTCTCGAACAGTTAGACTTTTATGTCTCGCTGTGCTCAAT 651
Qy 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArgSerPhe 207
Db 652 ATTGATGCTCATCATCTACACCTCGACCAAGACCGGATTTTGGAGAAAGACTCGCTCCACC 711
Qy 208 TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValserLysHisTrp 227
Db 712 CATACTGGATCTAGCTGATTTGGACACAGCCCAACAGAAATTTT---GATGCTGGTTGG 768
Qy 228 CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db 769 TGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCCGACAG 828
Qy 248 SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267
Db 829 TCTGAAAGGAGCAACCAAGCCCTGGCTGATTTCACTCCGCAACAACTCTCTTCCATCAAG 888
Qy 268 AlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArg 287
Db 889 GCATATCTGCACATCCATCTGCTACTCCCAATGATGATCTACCTTACTCATATGCTTAC 948
Qy 288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
Db 949 AAACCTCGGTGAGAACATCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAAGAACTT 1008
Qy 308 AspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
Db 1009 ---GCCCTCAGTCGACGCGCAACAGPACATATATGCGCGGAGCTTACAACTATATCCT 1065
Qy 328 AlaProGlyGlyLysAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 346
Db 1066 GCTGCTGGGGCTGTGACACTGGGCTTATGACCAAGGAATCAGATATCTCTTCAACC 1122
```

## RESULT 8

US-09-011-769A-38  
Sequence 38, Application US/09011769A  
Patent No. 6436691

## GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011.769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38

Alignment Scores:  
Pred. No.: 1.25e-71 Length: 1263  
Score: 639.00 Matches: 135  
Percent Similarity: 53.83% Conservative: 69  
Best Local Similarity: 35.62% Mismatches: 131  
Query Match: 33.44% Indels: 44  
DB: 4 Gaps: 7

US-09-980-881A-2 (1-360) x US-09-011-769A-38 (1-1263)

```
Qy 6 LeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla---PheGln 24
Db 4 CTCTTGTTCTGGGAGCTGTGGCCCTGCTCATCTGCTCATCTGCTGAGCATTGAA 63
Qy 25 SerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeuGlnAsn 44
Db 64 GCGCAGAGGTTGTCCTGTTAAGCTGAAGATGAAATACATTAACATAATCCGCGAG 123
Qy 45 LeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIleValLys 64
Db 124 TTGCCACGACGACGCCAGATTGACTTCTGGAAGCCAGATTCTGTGCACACAATCAACCT 183
Qy 65 LysLysGlnValHisPheValAsnAlaSerAspValaAspValaAsnValaHisLeu 84
Db 184 CACAGTACAGTTGACTTCCGTGTTAAAGCAGAAATGACTGTCTGCTGGAGAATGTTCTA 243
Qy 85 AsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIleGlnGln 104
Db 244 AAGCAGATGACTACATACAGTACTGATAAGCAACCTGAGAAATGTTGGTGGAGCT 303
Qy 105 GlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGlnTyrHis 124
Db 304 CAGTTTGTATGACCGGGTT-----CGTCAACAGGACACACAGTATGAGAAGTACAAAC 354
Qy 125 SerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAspMetLeu 144
Db 355 AAGTGGGAAACGATAGAGGCTTGGACTCAACAGTCCGCTGAGAAATCCAGCCCTCATC 414
Qy 145 ThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLysValser 164
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Db      415 TCTCGCAGTGTATCGAACACATTTTGAGGACGCGCTATTACCTCTCGAAGTT--- 471
QY      165 GlyLysGluGlnThrAlaLysAsnAlaIleTyrPheLeuAspCysGlyLeuHisAlaArgGlu 184
Db      472 GCGAAAGCTGGCAAAATTAAGCTGCCATTTTCATGGACTGTGGTTTCATGCCAGAGAG 531
QY      185 TrrPheSerProAlaPheCysLeuTrrPheIle----- 195
Db      532 TGGATTCTCTCGATTCTGCCAGCTGGTTTGTAAAGAGGCGTGTTCGTACCTATGGAGCT 591
QY      195 ----- 195
Db      592 GAGATCCAAAGTGCACAGAGCTTCTCGAACAGTTAGACTTTTATGCTCTGCTGTGCTCAAT 651
QY      196 -----GlyHis-----AsnArgMetTrrArgLysAsnArgSerPhe 207
Db      652 ATTGATGGCTACATCTACCTGGACCAAGACCGGATTTTGGAGAAAGACTCGCTCCACC 711
QY      208 TyrAlaAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLysHisTrrp 227
Db      712 CATACTGGATCTAGCTGCATTTGCCACAGACCCCAACAGAAATTTT---GATGCTGTTGG 768
QY      228 CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db      769 TGTGAATTTGGAGCTCTCGAAACCCCTGTGATGAACTTACTGTGGACCTGCCGACAG 828
QY      248 SerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLys 267
Db      829 TCTGAAAGGAAACCAAGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCCATCAAG 888
QY      268 AlaTrrIleSerMetHisSerTrrSerGlnHisIleValPheProTrrSerTrrThrArg 287
Db      889 GCATATCTGACAAATCACTGCTACTCCAAATGATGATCTACCTTACTCATATGCTTAC 948
QY      288 SerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIle 307
Db      949 ABACTCGGTGAGAACAAATCTGAGTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
QY      308 AspLysThrSerLysAsnThrArgTrrThrHisGlyHisGlySerGluThrLeuTrrLeu 327
Db      1009 ---GCCTCACTGACGCGCACCAAGTACACATATGCGCCCGGAGCTACAAATCTATCT 1065
QY      328 AlaProGlyGlyGlyAspAspTrrPheTrrAspLeuGlyLeuLysTrrSerPheThr 346
Db      1066 GCTGCTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTCACC 1122

```

RESULT 9

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US-08-860-882A-71
; Sequence 71, Application US/08860882A
; Patent No. 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAM, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUGH
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860.882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1284 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-860-882A-71

Alignment Scores:
Pred. No.: 1.18e-70 Length: 1284
Score: 631.50 Matches: 129
Percent Similarity: 54.57% Conservative: 68
Best Local Similarity: 35.73% Mismatches: 121
Query Match: 33.05% Indels: 43
DB: 2 Gaps: 6

US-09-980-881A-2 (1-360) x US-08-860-882A-71 (1-1284)
QY 23 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 42
Db 85 TTTGAGCGGAGAGTGTTCGTTTAACTGTAAGATGAAATCAACATTAACATAATC 144
QY 43 GlnAsnLeuThrThrTyrGluLeuValLeuTrrPheGlnProValThrAlaAspLeu 62
Db 145 CGCGAGTTGGCCAGCAGCAGCAGATTCGATTCGAAAGCCAGATTCGTCTACACAAATC 204
QY 63 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 82
Db 205 AAACCTCACAGTACAGTGTTCGTTTAAAGCAGAGATCTGCTCATCTGTGAGAT 264
QY 83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 102
Db 265 GTTCTAAAGCAGATGAACATACTAAGGTACTGATAAGCACTGAGAAATGTGGTG 324
QY 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTrrGluGln 122
Db 325 GAGGCTCAGTTTGATAGCGGGTT-----CGTGCAACAGGACACACATTTATGAGAAG 375
QY 123 TyrHisSerLeuAsnGluIleTyrSerTrrPheIleGluPheIleThrGluArgHisProA 142
Db 376 TACAACAAGTGGGAAACCGATGAGGCTTGGACTCAACAGTCCCACTGAGATTCAGGCC 435
QY 143 MetLeuThrLysIleHisIleGlySerPheGlyLysTrrProLeuTrrValLeuLys 162
Db 436 CTCATCTCTCGCAGTGTATCGAACACACATTTGAGGAGCGCGCTATTACCTCTCTGAAG 495
QY 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrrPheAspCysGlyIleHisAla 182
Db 496 GTT---GGCAAGCTGGCAAAATAAGCCTGCGCATTTTCATGAGACTGTGTTTCCATGCC 552
QY 183 ArgGluTrrPheSerProAlaPheCysLeuTrrPheIle----- 195
Db 553 AGAGAGTGGATTTCTCTCTGCTATTCCTGAGGAGGCTGTTTGTAAAGAGAGGCTGTTGTA 612
QY 195 ----- 195
Db 613 GGACGTGAGATCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGCTGCTGCTGTG 672
QY 196 -----GlyHis-----AsnArgMetTrrArgLysAsnArg 205

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Db 673 CTCATATTGATGGCTACATCTACACCTGGACCAAGCCGATTTTGGAGAAAGACTCGC 732
Qy 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
Db 733 TCCACCCATCTAGTCTAGCTGATTCGACAGACCCCAACAGAAATTTT--GATGCT 789
Qy 226 HisTrpCysGluGluAlaSerSerSerSerGluThrTyrCysGlyLeuTyr 245
Db 790 GGTGGTGTGAATGGAGCCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 849
Qy 246 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 265
Db 850 CGAGAGTCTGAAGAGACACAGCCCTGCTGATTCATCCGCAACAACTCTCTCC 909
Qy 266 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 285
Db 910 ATCAAGGCATATCTGACAACTCCTGCTACTCCCAATGATGATCTACCTTACTCATAT 969
Qy 286 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuAlaSerGluAlaValArg 305
Db 970 GCTTACAAACTCGGTGAGAACAACTGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1029
Qy 306 AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 325
Db 1030 GAACCTT---GCCCTACTCAGCGCCACCAAGTACACATATGCCCGGAGCTACACAAATC 1086
Qy 326 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 345
Db 1087 TATCTGCTGCTGGGGCTCTGACGACTGGCTTATGACCAAGGAATCAGATATTCCTTC 1146
Qy 346 Thr 346
Db 1147 ACC 1149
```

## RESULT 10

```
US-09-011-769A-55
; Sequence 55, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,769A
; FILING DATE: 13-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
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; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1284 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1272
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 352..1272
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-55
Alignment Scores:
Pred. No.: 1,18e-70 Length: 1284
Score: 631.50 Matches: 129
Percent Similarity: 54.57% Conservative: 68
Best Local Similarity: 35.73% Mismatches: 121
Query Match: 33.05% Indels: 43
DB: 4 Gaps: 6
US-09-980-881A-2 (1-360) x US-09-011-769A-55 (1-1284)
Qy 23 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 42
Db 85 TTTGAAGCGCAGAGAGGTGTTCCGTGTTAACGTTGAAGATGAAATACATTAACATAATC 144
Qy 43 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 62
Db 145 CGCGAGTTGGCCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTCCACCAAAATC 204
Qy 63 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 82
Db 205 AAACCTCAGAGTACAGTTGACTTCCTGTTAAAGCAGACAGATGACTGCTGTGGAGAA 264
Qy 83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 102
Db 265 GTTCTAAAGCAGAGTAACTACAACTACAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324
Qy 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 122
Db 325 GAGGCTCAGTTTGATAGCCGGGT-----CGTCAACAGCAGACAGATTATGAGAAG 375
Qy 123 TyrHisSerLeuAsnGluIleTyrSerTyrPheIleThrGluArgHisProAsp 142
Db 376 TACAACAGTGGGNAACGATAGAGGCTTGACTCAACAGTCCGCTGAGATCCAGCC 435
Qy 143 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 162
Db 436 CTCATCTCGCAGTGTATCGGAACCCACATTTTGGGGAGCGCGCTATTATTCCTCCTGAAG 495
Qy 163 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
Db 496 GTT---GGCAAGCTGGACAAATAAGCCTGCCATTTTCATGACTGTGGTTTCCATGCC 552
Qy 183 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 553 AGAGAGTGGATTTCTCTGTCATTTCTGCAGTGGTTTGTAGAGAGGCTGTTCTGTACCTAT 612
Qy 195 ----- 195
Db 613 GGAGCTGAGATCCAAAGTACAGAGCTTCTCGCAAGTTAGACTTTTATGTCTCCTGCTGTG 672
Qy 196 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 205
Db 673 CTCATATTTGATGGCTACATCTACCTCGGACCAAGAGCGGATTTTGGAGAAAGCTCGC 732
Qy 206 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerLys 225
```

D <sub>b</sub>	733	TCCACCCTACTCGATCTAGCTGCATTGGCACAGACCCCAAGAATAATTT---GATGCT	789
Q <sub>y</sub>	226	HieTrrpCysGluGluGlyAlaSerSerSerCysSerGluThrTrpCysGlyLeuYr	245
D <sub>b</sub>	790	GGTGTGGTGAAATTTGAGGCTCTCGAACCCCTGTGATGAALCTTACTGTGACACTGCC	849
Q <sub>y</sub>	246	ProGluSerGluProGluVallyAlaValAlaSerPheLeuArgAraAsnIleAsnGln	265
D <sub>b</sub>	850	GCAGAGTCGTAAANGAGCACCAGGCCCTGGCTGATTTTCATCCGCAACAACCTCTCTCC	909
Q <sub>y</sub>	266	IleLysAlaTyrlleSerMetHisSerTyrrSerGlnHisIleValPheProTyrrSerTyrr	285
D <sub>b</sub>	910	ATCAAGGCATATCTGACAATCCAATCGTACTCCCAAATGATGATCTACCTTACTCATAT	969
Q <sub>y</sub>	286	ThrArGerLyssSerLyssAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg	305
D <sub>b</sub>	970	GCTTTACAAACTCGGTGAGACAANTGCTGAGTGAATGCCCTGGCTAAAGCTACTGTGAAA	1029
Q <sub>y</sub>	306	AlaIleAspLyssThrSerLyssAsnThrArgTyrrThrHisGlyHisGlySerGluThrLeu	325
D <sub>b</sub>	1030	GAACTT---GCCCTACTGCACGGCACCACCAAGTACACATATATGCCCGGAGCTACACAACT	1086
Q <sub>y</sub>	326	TyrLeuAlarProGlyGlyGlyAspAspTrlileTyrrAspLeuGlyIleIleTyrrSerPhe	345
D <sub>b</sub>	1087	TATCCTGCTGTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATTCAGATATTCTTC	1146
Q <sub>y</sub>	346	Thr 346 	
D <sub>b</sub>	1147	ACC 1149 	

## RESULT 11

```

US-09-171-945-124
; Sequence 124, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-124

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Alignment Scores:		
Pred. No.:	3.59e-69	Length: 2154
Score:	623.00	Matches: 132
Percent Similarity:	53.40%	Conservative: 72
Best Local Similarity:	34.55%	Mismatches: 134
Query Match:	32.60%	Indels: 32 44
DB:	3	Gaps: 7

US-09-980-881A-2 (1-360) X US-09-171-945-124 (1-2154)

Qy	3	Leu	Cys	Ser	Leu	Ala	Val	Leu	Val	Pro	Ile	Val	Leu	Phe	Cys	Glu	Gln	His	Val	Phe	Ala	22	
		:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::	:::		
Db	1	ATG	TTC	GCA	CTC	TGG	TTC	TGG	TGAC	TCT	GGC	CCT	GGC	ATC	TCT	GC	T	CAT	CAT	CTG	TGG	TGAG	60

23	QY	---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal	41
61	DB	CACTTTGAAGGGCAGAGAGGTTCCTGTTAACTGTAAGATGAAATACATTAACATA	120
42	QY	LeuGlnAsnLeuThrThrTyrrGluIleValLeuTrrpGlnProValThrAlaAspLeu	61
121	DB	ATCCGGGAGTTGGCCAGCAGCACCAGATTGACTTCTGGAAGCCAGATTCTGTGCACAA	180
62	QY	IleValLysLysGlnValHisPheValAsnAlaSerAspValAsnValLys	81
181	DB	ATCAAACTCACAGTACAGTTGACTTCGTTGTTAAAGCAGAGATACTGTCACCTGGG	240
82	QY	AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu	101
241	DB	AATGTCTTAAAGCAGATGACTACATACAGGTACTGATAGCAACCTGAGAAATGTG	300
102	QY	IleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrGlu	121
301	DB	GTGGAGGCTCAGTTTGATAGCCGGTT-----CGTCAACAGCAGACAGATTATGAG	351
122	QY	GlnTyrrHisSerLeuAsnGluIleTyrrSerTrrpIleGluPheIleThrGluArgHisPro	141
352	DB	AAGTACAAACAGTGGGAACGATAGAGGCTTGGACTCAACAGTCGCCACTGAGAATCCA	411
142	QY	AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrValLeu	161
412	DB	GCCTCATCTCTCGCAGTGTATTCGAACACATTTGAGGAGCGCTATTTACTCTCTG	471
162	QY	LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrrpIleAspCysGlyIleHis	181
472	DB	AAAGTT---GGCAAGCTGCACAAATAAGCTGCCATTTTCATGGACTGTGGTTCCAT	528
182	QY	AlaArgGluTrrpIleSerProAlaPheCysLeuTrrpPheIle-----	195
529	DB	GCCAGAGTGGATTCTCTGCACTTCGCCAGTGGTTGTTAAGAGAGGCTGTTTCGTACC	588
195	QY	-----	195
589	DB	TATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGCTCGCT	648
196	QY	-----GlyHis-----AsnArgMetTrrpArgLysAsn	204
649	DB	GTGCTCAATATTGATGGCTACATCTACCTGGACCAAGCCGATTTGGAGAAAGACT	708
205	QY	ArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSer	224
709	DB	CGCTCCACCACATCTGGATCTAGCTGATTGGCACAGACCCCAACAGAAATTTT---GAT	765
225	QY	LysHisTrrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrrCysGlyLeu	244
766	DB	GCTGGTTGGTGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCT	825
245	QY	TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsn	264
826	DB	CGCCGAGAGTCTGAAAAGGAGACCAAGCCCTGGCTGATTTCATCCGCAACAACTCTCT	885
265	QY	GlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPheProTyrrSer	284
886	DB	TCCATCAAGGATATCTGACAATCCACTCGTACTCCCAATATGATGATCTACCCCTTACTCA	945
285	QY	TyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAlaVal	304
946	DB	TATGCTTCAAACTCGGTGAGAACATGCTGATTGAATGCCCTGGCTAAAGCTACTGTG	1005
305	QY	ArgAlaIleAspLysThrSerLysAsnThrArgTyrrThrHisGlyHisGlySerGluThr	324
1066	DB	AAAGAACTT---GCCCTACTCGCGGCAACCAAGTACACATATGGCCGGGAGCTACAACA	1062
335	QY	LeuTyrrLeuAlaProGlyGlyLysAspTrrpIleTyrrAspLeuGlyIleLysTyrrSer	344
1063	DB	ATCTATCCTTCTGTGGGACTTCTTAAGAGACTGGGCTTATGACCAAGGAATCAGATATTCC	1122
345	QY	PheThr	346







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; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-675-305-9

Alignment Scores:
Pred. No.: 4,54e-68 Length: 1311
Score: 611.50 Matches: 141
Percent Similarity: 50.36% Conservative: 69
Best Local Similarity: 33.81% Mismatches: 135
Query Match: 32.00% Indels: 72
DB: 4 Gaps: 11

US-09-980-881A-2 (1-360) x US-09-675-305-9 (1-1311)
Qy 1 MetLysLeuCys-----SerLeuAlaValLeuValProfileValLeuPheCysGluGln 18
Db 43 CTGCCTCTTTCGTGGCTCTTTTGAAGATTCTGCAACCG-----GGGCACAGC 90
Qy 19 HisValPhe-----AlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSer 36
Db 91 CACCTTTATAACAACCGCTGCTGGTATAAGTGATAAGATTTATTTCCCAAAACAGAA 150
Qy 37 ArgGlnValGlnValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnPro 56
Db 151 GAGGAAGCATATGCACTCGAAGAAATATCCTATCAACTTAAGTGGAGCTGTGGCAGGCC 210
Qy 57 ValThrAlaAspLeuIleValLys-----LysLysGlnValHisPhePheValAsnAla 74
Db 211 AGCAGTATCTCTATGTATCAGAGGGAACAGTTACTGTATGTCATATCCCCAAATAGT 270
Qy 75 SerAspValAspAsnValLysAlaHisIleuAsnValSerGlyIleProCysSerValLeu 94
Db 271 TCCCGAGCC-----CTGTTAGCCTTCTTACAGGAAGCCACATCCAGTACAAAGGTCTCT 324
Qy 95 LeuAlaAspValGluAspLeuIleGlnGlnIleSerAsnAspThrValSerProArg 114
Db 325 ATAGAAGATCTTCAGAAACACTGGAGAAGGGAAGCAGCTTGCACACCAGAGAACCAG 384
Qy 115 AlaSerAlaSer-----TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyr 132
Db 395 AGATCCCTCTCGGATATAATATGAGTTTATCACTCTCTTAGAGAAATTCAAAATTGG 444
Qy 133 IleGluPheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSer 152
Db 445 ATGCATCATCTGAATAAAACTCACTCAGGCCTCAITTCACATGTCTCTATTTGGAAGATCA 504
Qy 153 PheGluLysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsn 172
Db 505 TATGAGGGAAGATCTCTTTTATTTTAAAGCTG---GGCAGACGATCATCGACTCAAAAGA 561
Qy 173 AlaIleTyrIleAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeu 192
Db 562 GCTGTTTGATAGACTGTGTTATTCATGCAAGAGATGGATTGGTCTGCTGCTTTTGTCTAG 621
Qy 193 TrpPheIle----- 195

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Thu Oct 28 07:16:11 2004

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Best Local Similarity: 44.48%      Mismatches: 72
Query Match: 31.61%      Indels: 41
DB: 2      Gaps: 5

US-09-980-881A-2 (1-360) x US-08-782-760-5 (1-927)

QY 115 AlaSerAlaSerTyTyGluGlnTyHisSerLeuAsnGluLeuTySerTrpIleGlu 134
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Db 1 GCAAGTGGACACAGCTACACCAAGTACAACTGGGAAACGATTGAGCGTGGATTCAA 60
   |||||

QY 135 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 154
   |||||
Db 61 CAAAGTTGCCACTGATAATCCACACCTTGTCACTCAGAGCGTCAATTGGAAACCAATTGAA 120
   |||||

QY 155 LysTyProLeuTyValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 174
   |||||
Db 121 GGACGTAAACATGTATGTCTCAAGATT--GGTAAACTAGACCGAATAAGCCTGCCATC 177
   |||||

QY 175 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 194
   |||||
Db 178 TTATCGATTGTGGTTTCCATGCAAGAGAGTGGAATTTCTCTGCATTTCTGCAGTGGTTT 237
   |||||

QY 195 Ile----- 195
   |||

Db 238 GTGAGAGAGGCTGTCGTTACTATAATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297
   |||

QY 196 -----GlyHis----- 197
   |||

Db 298 CTGGATTTCATGTTCTGCTGTGCTCAACATTGATGGCTATGCTCTACACCTGGACTAAG 357
   |||||

QY 198 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 217
   |||||
Db 358 GACAGAATGTGGAGAAAACCGCTCTACTATGGCTGGGAAGTCTCGTGTGGGTAGAC 417
   |||||

QY 218 LeuAsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 237
   |||||
Db 418 CCCAACAGGAATTTT--AATGCTGGCTGGTGTGAAGTGGAGCTTCTCGAGTCCCTGC 474
   |||||

QY 238 SerGluThrTyrcysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSer 257
   |||||
Db 475 TCTGAAACTTACTGTGGACCGCCAGAGTCTGMAAAAGAGACAAAGCCCTGGCAGAT 534
   |||||

QY 258 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTyTrSerGln 277
   |||||
Db 535 TTATCCGCAACAACTCTCCACCATCAAGGCTCTGACCATCCACTCATCTACTACAG 594
   |||||

QY 278 HisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluLeuSer 297
   |||||
Db 595 ATGATGCTCTACCTTACTCTCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654
   |||||

QY 298 LeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyThr 317
   |||
Db 655 GCCCTGGTGAAGGTGGCGCAAGAGCTT--GCCACTCTGCATGGCACCAAGTACACA 711
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QY 318 HisGlyHisGlySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTy 337
   |||||
Db 712 TATGGCCCGAGGAGCTACAAATCTATCTCTGCTGGGGGATCTGACGACTGCTCTTAT 771
   |||||

QY 338 AspLeuGlyIleLysTySerPheThrSerAsnProValGluLysLeuLeuProLeu 357
   |||||
Db 772 GATCAGGGATCAATATTCCTTTTACCTTTTGAACCT--CCGGGATACAGGCTTCTTTGGCTT 830
   |||||

QY 358 Ser 358
   |||
Db 831 TCT 833
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Search completed: October 27, 2004, 02:01:06  
Job time : 109.576 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:54:23 ; Search time 1724.49 Seconds  
(without alignments)  
1070.424 Million cell updates/sec

Title: US-09-980-881A-2  
Perfect score: 1911  
Sequence: 1 MKCLSLAVLPVFLCEQHV.....IKSPTSPPVKKLPLSLK 360

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40 cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ext -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0980881.0cgn\_1\_1034.0runat\_26102004\_084115\_7269  
-NCPU=6 -ICPU=3 -NO MMAP -LARGUEYERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:
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- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:
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- 18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1849.5	96.8	1625	9	US-09-813-133A-1	Sequence 1, Appli
2	1849.5	96.8	1625	14	US-10-212-877-1	Sequence 1, Appli
3	1832	95.9	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	1808.5	94.6	1344	16	US-10-115-479-69	Sequence 69, Appl
5	1808.5	94.6	1743	16	US-10-115-479-67	Sequence 67, Appl
6	1729	90.5	1272	15	US-10-379-836-1	Sequence 1, Appli
7	1439.5	75.3	1037	16	US-10-115-479-63	Sequence 63, Appl
8	1393.5	72.9	1132	16	US-10-115-479-65	Sequence 65, Appl
9	889	46.5	1400	9	US-09-925-302-24	Sequence 24, Appl
10	889	46.5	1400	10	US-09-925-302-24	Sequence 24, Appl
11	623	32.6	2154	9	US-09-910-059-124	Sequence 124, App
12	621.5	32.5	1332	9	US-09-954-456-1141	Sequence 1141, Ap
13	620.5	32.5	1633	15	US-10-341-434-187	Sequence 187, App
14	620.5	32.5	1740	14	US-10-116-802-95	Sequence 95, Appl
15	619.5	32.4	1254	14	US-10-229-546-3	Sequence 3, Appli
16	619.5	32.4	1622	14	US-10-229-546-1	Sequence 1, Appli
17	619.5	32.4	1622	15	US-10-429-802-21	Sequence 21, Appl
18	619.5	32.4	1622	16	US-10-430-503-12	Sequence 12, Appl
19	619.5	32.4	1622	16	US-10-262-511-71	Sequence 71, Appl
20	619.5	32.4	1622	16	US-10-641-643-1020	Sequence 1020, Ap
21	611.5	32.0	1302	17	US-10-477-515-1	Sequence 1, Appli
22	611.5	32.0	1311	13	US-10-200-344-9	Sequence 9, Appli
23	611.5	32.0	1993	15	US-10-274-639-33	Sequence 33, Appl
24	611.5	32.0	1993	16	US-10-333-574-33	Sequence 33, Appl
25	609.5	31.9	1907	18	US-10-757-262-127	Sequence 127, App
26	591	30.9	416	9	US-09-960-352-14595	Sequence 14595, A
27	564	29.5	2128	13	US-10-200-344-13	Sequence 13, Appl
28	563	29.5	1125	9	US-09-888-615-2	Sequence 2, Appli
29	563	29.5	1332	15	US-10-176-306-75	Sequence 75, Appl
30	563	29.5	1603	15	US-10-176-306-73	Sequence 73, Appl
31	556	29.1	1826	15	US-10-252-157-453	Sequence 453, App
32	546	28.6	1200	14	US-10-200-910-7	Sequence 7, Appli
33	546	28.6	1200	18	US-10-843-130-7	Sequence 7, Appli
34	543	28.4	1870	9	US-09-910-059-112	Sequence 112, App
35	543	28.4	1870	17	US-10-608-710-3	Sequence 3, Appli
36	528.5	27.7	1050	13	US-10-200-344-11	Sequence 11, Appl
37	527.5	27.6	991	16	US-10-383-201-93	Sequence 93, Appl
38	519.5	27.2	1260	16	US-10-257-174-16	Sequence 16, Appl
39	519.5	27.2	1311	14	US-10-200-910-5	Sequence 5, Appli
40	519.5	27.2	1311	16	US-10-257-174-15	Sequence 15, Appl
41	519.5	27.2	1311	17	US-10-451-821-1	Sequence 1, Appli
42	519.5	27.2	1311	18	US-10-843-130-5	Sequence 5, Appli
43	519.5	27.2	1348	16	US-10-072-012-315	Sequence 315, App
44	519.5	27.2	1641	17	US-10-381-820A-5	Sequence 5, Appli
45	514.5	26.9	1295	17	US-10-363-829-148	Sequence 148, App

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1  
Alignment Scores:

Pred. No.: 4,278-219 Length: 1625  
Score: 1849.50 Matches: 355  
Percent Similarity: 94.18% Conservative: 1  
Best Local Similarity: 93.92% Mismatches: 4  
Query Match: 96.78% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

Qy 1 MetLysLeuCysSerLeuAlaValLeuProLleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAAGCTTTGAGAGCTTGCAGCTTCTGTACCCATTTCTCTCTCTGTGAGCAGATGTC 76

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTGCGGTTTACAGAGTGGCAGATTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 136

Qy 41 ValLeuGlnAenLeuThrThrThrGluLeuValLeuTyrGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGATCTTACTACACATATGAGATTTGTTCTGCGAGCCGGTAACAGCTGAC 196

Qy 61 LeuLeuValLysLysGlnValHisPheValAenAlaSerAspValAsnVal 80  
Db 197 CTTATTGTGAAGAAAACAGTCCATTTTGTAAATGCATCTGATGTCGACATGTG 256

Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGAATTCATGTCAGTGTCTGCTGGCAGATGTGGAAGAT 316

Qy 101 LeuLeuGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTACAGCAGATTTTCAACACACAGATGAGCCCGGAGCTCCGATCGTACTAT 376

Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpLleGluPheThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATCTATCTTGGATAGATTTATAACTGAGAGGAT 436

Qy 141 ProAspMetLeuThrLysLleHisLleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CCTGATATGCTTACAAAAATCCATATGATGCTCTCATTTGAGAGTACCCACTCTATGT 496

Qy 161 LeuLysValSerGlyLysGlnThrAlaLysAenAlaLeuTyrPheAspCysGlyLeu 180  
Db 497 TTAAGGTTTCTGGAAGAAACACACAGCCAAAAATGCCATATGATGATGTGGAATC 556

Qy 181 HisAlaArgGluTyrPheSerProAlaPheCysLeuTyrPheLleGlyHisAsnArgMet 200  
Db 557 CATGCCAGAGATGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAATAATCGAATG 616

Qy 201 TrpArgLysAenArgSerPheTyrAlaAenAenHisCysLleGlyThrAspLeuAsnSer 220  
Db 617 TGGAGAAAGAACCGTTCTTCTATCGAACCAATCATTTGATCGGAAACAGCTGAAATAGG 676

Qy 221 AenPheValSerLysHisTyrCysGluGluGlyAlaSerSerSerCysSerGluThr 240  
Db 677 AACTTTGCTTCCAAACACTGGTGTGAGGAGTGTATCCAGTTCTCTATGCTCGGAACC 736

Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
Db 737 TACTGTGACATTTATCTGAGTCAGAACCAAGGAGGAGTGTGCTGCTGCTGCTGCTGCTG 796

Qy 261 ArgAenLleAenGlnLleLysAlaTyrLleSerMetHisSerTyrSerGlnHisLleVal 280  
Db 797 AGAATATCAACAGATTTAAAGCATATCATGATGATGATGATGATGATGATGATGATGATG 856

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Db 857 TTTCCATATCTCTATACAGAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 916

Qy 301 SerGluAlaValArgAlaLleAspLysThrSerLysAenThrArgTyrThrHisGlyHis 320  
Db 917 AGTGAAGCAGTTCTGCTATTGAGAAAATTTAGTAAATAATACAGGTATACACATGCGCAT 976

Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyCysAspTyrPheTyrAspLeuGly 340  
Db 977 GGCTCAGAAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATGATGATGATGATGATG 1036

Qy 341 IleLysTyrSerPhe----- 345  
Db 1037 ATCAAAATATTCGTTTACAATGAACCTTCGAGATACGGGCACATACGATTTCTGCTCCG 1096

Qy 346 -----ThrSerAenProValGluLysLeuLeuProLeuSerLeuLys 360  
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RESULT 2  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; CURRENT FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 09/813,133  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

Alignment Scores:  
Pred. No.: 4,278-219 Length: 1625  
Score: 1849.50 Matches: 355  
Percent Similarity: 94.18% Conservative: 1  
Best Local Similarity: 93.92% Mismatches: 4  
Query Match: 96.78% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-2 (1-360) x US-10-212-877-1 (1-1625)

Qy 1 MetLysLeuCysSerLeuAlaValLeuProLleValLeuPheCysGluGlnHisVal 20  
Db 17 ATGAAGCTTTGAGAGCTTGCAGCTTCTGTACCCATTTCTCTCTCTGTGAGCAGATGTC 76

Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 77 TTGCGGTTTACAGAGTGGCAGATTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 136

Qy 41 ValLeuGlnAenLeuThrThrThrGluLeuValLeuTyrGlnProValThrAlaAsp 60  
Db 137 GTTCTACAGATCTTACTACACATATGAGATTTGTTCTGCGAGCCGGTAACAGCTGAC 196

Qy 61 LeuLeuValLysLysGlnValHisPheValAenAlaSerAspValAsnVal 80  
Db 197 CTTATTGTGAAGAAAACAGTCCATTTTGTAAATGCATCTGATGTCGACATGTG 256

Qy 81 LysAlaHisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 257 AAAGCCCATTTAAATGTGAGCGAATTCATGTCAGTGTCTGCTGGCAGATGTGGAAGAT 100

Qy 101 LeuLeuGlnGlnGlnSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 317 CTTATTACAGCAGATTTTCAACACACAGATGAGCCCGGAGCTCCGATCGTACTAT 120

Qy 121 GluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpLleGluPheThrGluArgHis 140  
Db 377 GAACAGTATCACTCACTAAATGAATCTATCTTGGATAGATTTATAACTGAGAGGAT 140

Qy 141 ProAspMetLeuThrLysLleHisLleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 437 CCTGATATGCTTACAAAAATCCATATGATGCTCTCATTTGAGAGTACCCACTCTATGT 160

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Db 437 CCTGATATGCTTACAAAAATCCACATGGATCCTCATTTGAGAGTACCCTCTATGTT 496
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 497 TTAAGGTTTCTGGAAGAAACAAGCAGCAAAAATGCCATATGATGATGACTGTGGAATC 556
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMet 200
Db 557 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTGTTCTATGGCCATTAATCGAATG 616
Qy 201 TrpArgLysAsnArgSerPheTrpAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
Db 617 TGGAGAAAGAACCGTCTTCTTATGCGAACATCATTTGATCGGAACAGACCTGATAGG 676
Qy 221 AsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThr 240
Db 677 AACTTTGCTTCCAAACACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAAACC 736
Qy 241 TyrCysGlyLeuTrpProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260
Db 737 TACTGTGGAATTATCTCTGAGTCAGAACCCAGAGAGTGAAGCGAGTGGCTAGTTCTTTGAGA 796
Qy 261 ArgAsnIleAsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGlnHisIleVal 280
Db 797 AGAATATACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTG 856
Qy 281 PheProTrpSerTrpThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300
Db 857 TTTCCATATCTCTATACAGAGTAAAGCAAAAGACCATGAGGAACATGCTCTCTAGTAGCC 916
Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTrpThrHisGlyHis 320
Db 917 AGTGAAGCAGTTCGTCTATTGAGAAAAATTAGTAAATAATACCAAGGTATACATGCGCCAT 976
Qy 321 GlySerGluThrLeuTrpLeuAlaProGlyGlyAspAspTrpIleTrpAspLeuGly 340
Db 977 GGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGGAGCATGGATCTATGATTGGGC 1036
Qy 341 IleLysTrpSerPhe----- 345
Db 1037 ATCAATATATCGTTTACAAATTGAATTCGAGATACGGGCACATACGGATTCTTGTGCGCG 1096
Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1097 GAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1148
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RESULT 3

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US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396
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Alignment Scores:
Pred. No.: 7,12e-217 Length: 1728
Score: 1832.00 Matches: 357
Percent Similarity: 86.27% Conservative: 1
Best Local Similarity: 86.02% Mismatches: 2
Query Match: 95.87% Indels: 55
DB: 9 Gaps: 2
US-09-980-881A-2 (1-360) x US-09-880-107-2396 (1-1728)
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 20 ATGAAGCTTTGCAGCTTTCAGCTCTTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 79
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaIleLeuProArgThrSerArgGlnValGln 40
Db 80 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTCTCTTAGAACCTCTAGGCAAGTTCAA 139
Qy 41 ValLeuGlnAsnLeuThrThrTrpTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 140 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGCGACCGGTAAACAGCTGAC 199
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 200 CTTATTGTGAAGAAAAACAAGTCCCATTTTTTTGTAAATGCAATCTGATGTCGACCAATGTG 259
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 260 AAAGCCCATTTAAATGTGAGCGGAATTCATGAGTGTCTTCTGCGACAGCTGGAGAT 319
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTrpTrp 120
Db 320 CTTATTCAACAGCAGATTTCCAAACGACACAGTCAGCTCCGAGCTCCGCACTGCTACTAT 379
Qy 121 GluGlnTrpHisSerLeuAsnGluIleTrpSerTrpIleGluPheIleThrGluArgHis 140
Db 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAAATTTATACTGAGAGGCAT 439
Qy 141 ProAspMetLeuThrLysIleHisGlySerSerPheGluLysTrpProLeuTrpVal 160
Db 440 CCGTATATGCTTACAAAAATCCACATTTGGATCTCATTTTGAGAAGTACCACCTCTATGTT 499
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 500 TTAAGGTTTCTGGAAGAAACAAGCAGCAAAAATGCCATATGATGATGACTGTGGAATC 559
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db 560 CATGCCAGAGATGGATCTCTCTGCTTTCTGCTTGTGTTCTATAGGCCATATAACTCAA 619
Qy 197 ----- 197
Db 620 TTCTATGGGATAATAGGCAATATACCAATCTCTCGAGGCTGTGGATTTCATGTTATG 679
Qy 198 -----AsnArgMetTrpArgLys 203
Db 680 CCGGTGGTTAATGTGACCGGTTATGACTACTCATGCAAAAAGAAATCGAATGTGGAGAAG 739
Qy 204 AsnArgSerPheTrpAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 740 AACCGTTCTTCTATCGGAACAATCATTTGCATCGGAACAGACCTGAAATAGGAACCTTTGCT 799
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTrpCysGly 243
Db 800 TCCAAACACTGGGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGA 859
Qy 244 LeuTrpProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263
Db 860 CTTTATCTCTGAGTCAGAACCAAGAGTGAAGGCTAGTGTCTTTGAGAAGAAATATC 919
Qy 264 AsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGlnHisIleValPheProTrp 283
Db 919 CTTTATCTCTGAGTCAGAACCAAGAGTGAAGGCTAGTGTCTTTGAGAAGAAATATC 919
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Db 920 AACAGATTAAAGCATACATCAGCATGATTCATACACTCCAGCATATAGTGTTCATAT 979  
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303  
Db 980 TCCTATACACGAAGTAAAGCAAGAACCATCAGGAACCTGTCTAGTAGCCAGTGAAGCA 1039  
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323  
Db 1040 GTTCGTGCTATTGTAAGAACTAGTAAATAATACAGGTATACACATGGCCATGGCTCAGAA 1099  
Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyValAspAspTrrPileTyrAspLeuGlyLysTyr 343  
Db 1100 ACCATTATACCTAGCTCCTGGAGTGGGACGATGGATCTATGATTTGGGCATCAATAT 1159  
Qy 344 SerPhe-----Th 346  
Db 1160 TCGTTTACATTGAACCTTCGAGATACGGGCACATACGGATTCTTGCTCCGGAGGTTTAC 1219  
Qy 346. rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360  
Db 1220 ATCAAAACCACCTGTAGAGAAAGCTTTTCCCGCTGTCTCTAATA 1262

## RESULT 4

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zethusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shamkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 69  
; LENGTH: 1344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (31)..(1315)  
US-10-115-479-69  
Alignment Scores:  
Pred No.: 3,93e-214 Length: 1344  
Score: 1808.50 Matches: 355  
Percent Similarity: 84.76% Conservative: 1  
Best Local Similarity: 84.52% Mismatches: 4  
Query Match: 94.64% Indels: 60  
DB: 16 Gaps: 3  
US-09-980-881a-2 (1-360) x US-10-115-479-69 (1-1344)  
Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
Db 31 ATGAAGCTTTGCAGCCTTGAGTCTCTGTATCCCATTTCTCTCTCTGTGAGCAGCATGTC 90  
Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
Db 91 TTCGCGTTTCAGAGTGGCCAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAA 150  
Qy 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAsp 60  
Db 151 GTTCTACAGATCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 210  
Qy 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80  
Db 211 CTATTCTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTGCAATGTG 270  
Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
Db 271 AAGCCCATTTAAATGTGAGCGGAATTCATGCAAGTGTCTTGTGGCAGAGCTGGAAGAT 330  
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
Db 331 CTATTTCACAGCAGATTTCCACAGCACAGTCAGCCCCCGAGCCTCCGCACTGCTACTAT 390  
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
Db 391 GAACAGTATCACTCACTAAATGAAATCTATTCTTTGGATAGAAATTTATACTGAGAGGCAT 450  
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
Db 451 CCTGATATGCTTACAAAAATCCACATTTGGATTCCTCATTTGAGAAGTACCCACTCTATGTT 510  
Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175  
Db 511 TTTAAAGGGTTTCTTTGAGCAGGTTTCTTGAAAAAGAACAAAGCAGCAAAATGCCATATGG 570  
Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195  
Db 571 ATTGACTGTGAATCCATGCCAGAGATGGATCTCTCTGCTTTCTGCTTTGTGTTTATA 630  
Qy 196 GlyHis----- 197  
Db 631 GGCCTATTAACCTCAATTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTTGTG 690  
Qy 198 -----Asn 198  
Db 691 GATTTCATGTTATGTCGGTGGTTAATGTGATGGTTTATGACTACTCATGAGAAAAAGAAAT 750



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QY 199 ArgMetTrrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
DB 751 CGAATGTGGAGAAAGAACCGTTCTTCTAATGCGAACATCATGTGCGAACACACCTG 810
QY 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238
DB 811 AATAGGAACCTTTGCTTCCAAACACATGGTGTGAGGAAGGTGCATCCAGTTCTCATGCTCG 870
QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
DB 871 GAAACCTACTGTGGACTTTTCTCTAGTCAGTCAAGAACCAAGAGTGAAGCAGTGGCTAGTTTC 930
QY 259 LeuTyrArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
DB 931 TTGAGAAGAAATATCAACAGATTAAAGCATATCAATCAGCATGCATTCATCTCCAGCAT 990
QY 279 IleValPheProTyrSerTyrThrArgSerLysLysSerLysAspHisGluGluLeuSerLeu 298
DB 991 ATAGTGTTCCTATATCTTATACAGAACTAAAGCAAGACCATGAGGAACCTGTCTCTA 1050
QY 299 ValAlaSerGluAlaValAlaGlnIleAspLysThrSerLysAsnThrArgTyrThrHis 318
DB 1051 GTAGCCAGTGAAGCAGTCTGTCTATTGAGAAAATAGTAAAAATACCAGGTATACACAT 1110
QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
DB 1111 GGCCATGGCTCAGAACCTTATACCTAGCTCTCTGGAGGTGGGAGCAGATTGGATCTATGAT 1170
QY 339 LeuGlyIleLysTyrSerPhe----- 345
DB 1171 TTGGGCATCAATATTCGTTTACAAATTGAACCTCGAGATACGGGCACATACGGAATTCCTG 1230
QY 346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
DB 1231 CTGCGCGAGGCTTACATCAAAACCCACCTCTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1288
RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malvanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
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; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
; US-10-115-479-67

Alignment Scores:
Pred. No.: 6,06e-214 Length: 1743
Score: 1808.50 Matches: 355
Percent Similarity: 84.78% Conservative: 1
Best Local Similarity: 84.52% Mismatches: 4
Query Match: 94.64% Indels: 60
DB: 16 Gaps: 3

US-09-980-881A-2 (1-360) x US-10-115-479-67 (1-1743)
QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
DB 20 ATGAAGCTTTGCAGCCTTGCAGCTCTCTGTACCATTTGTTCTCTCTGTGAGCAGCATGTC 79
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
DB 80 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTAGAACCTCTAGGCAAGTTCAA 139
QY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
DB 140 GTTCTACAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGAC 199
QY 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAsnVal 80
DB 200 CTTATTGTGAAGAAAAACAAGTCCATTTTTTTTGTAAATGTCATCTGATGCGACAATGTG 259
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuAlaAspValGluAsp 100
DB 260 AAAGCCCATTTAAATGTGAGCGGAATTCATGCAGTGTCTGTGTCGACAGCTGGGAAGAT 319
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
DB 320 CTTATTCAACAGCAGATTTCACACGACACACAGTCAGCCCGCGCTCCGATCGTACTAT 379
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
DB 380 GAACAGTATCACTCACTAAATGAAATCTATTCTTGTGATAGAAATTTATACTGAGAGGCAT 439
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
DB 440 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTGAGAAAGTACCACCTCTATGTT 499
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QY 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175
Db 500 TTAAGGGTTCCTTTGAGCAGGTTCTGGAAAAAGAACAGCAGCCAAAAATGCCATATGG 559

QY 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195
Db 560 ATTGACTGGGATCCATCCAGCAAGATGATCTCTCTGCTTCTGCTTCTGTTGTTTATA 619

QY 196 GlyHis----- 197
Db 620 GGCCATAATAACTCAATTCATGGGATAATAGGGCAATATACCAATCTCTCGAGGCTTGTG 679

QY 198 -----Asn 198
Db 680 GATTTCATGTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCATGGAAAAAGAAAT 739

QY 199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218
Db 740 CGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTTGCATCGGAACAGACCTG 799

QY 219 AsnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238
Db 800 AATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCG 859

QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPhe 258
Db 860 GAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGCAGTGGCTAGTTTC 919

QY 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278
Db 920 TTGAGAAGAAATATCAACAGATTAAAGCATATACATCAGCATGCATTCATCTCCAGCAT 979

QY 279 IleValPheProTyrSerTyrThrArgSerLysLysAspHisGluGluLeuSerLeu 298
Db 980 ATAGTGTTCATATTCCTATACAGAAAGTAAAGCAAGACCATATGAGGAACTGTCTCTA 1039

QY 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318
Db 1040 GTAGCAGTGAAGCAGTTCGTGCTATTGAGAAATATTAGTAATAATATACCAGGTATACAT 1099

QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAsp 338
Db 1100 GSCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGAT 1159

QY 339 LeuGlyIleLysTyrSerPhe----- 345
Db 1160 TTGGGCATCAAAATATTCGTTTACAATTTGAACCTTCGAGATACGGGCACATACGGATTCTTG 1219

QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1220 CTGCCGAGGCGGTATACATCAACCCACCTGTAGAGAAAGCTTTTGCCGCTGTCTCTANAA 1277

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## RESULT 6

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US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: (1)...(1269)
US-10-379-836-1

Alignment Scores:
Pred. No.: 2,79e-204 Length: 1272
Score: 1729.00 Matches: 338
Percent Similarity: 83.37% Conservative: 8
Best Local Similarity: 81.45% Mismatches: 14
Query Match: 90.48% Indels: 55
DB: 15 Gaps: 2

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US-09-980-881A-2 (1-360) x US-10-379-836-1 (1-1272)

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QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 1 ATGAAGCTTTGCAGCTTTGCAGTCTTGTAGTACCCATTGTTCTCTCTGTGACGACGATGTC 60

QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGln 40
Db 61 TTCGGCTTCAGAGTGGCCAGGTTCTAGTGTCTTCTCTAGAACCTCTAGGCAAGTTCAA 120

QY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 121 GTGCTACAGAATCTTACTACAAATATGAGATTGTTCTCTGCGACGCGGTAAACGCGGAC 180

QY 61 LeuIleValLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVal 80
Db 181 CTTATTGAGAAGAAAAACAAGTCCATTTTTTTGTAATTCATCTGATGTGCAAAATGTG 240

QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 241 AAAGCCCATTTAATGTGAGCGGAATTCATGTCAGTGTCTCTGCTGGCAGATGTGGAAGAT 300

QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 301 CTTATTCAACAGCAGATTTCCACGACACATGTCAGCCCGCAGGCTCCGCACTCGTACTAT 360

QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 361 GAAACAGTATCACTCACTAAATGAAATCTATTCTTTGGATGAACTTATAACTGAGAAGTAT 420

QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 421 CCTGATATGCTTACAAAAATCCACATTTGGATCCTCTCTATGAGAAGACCCCACTTTATGTT 480

QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 481 TTAAGGTTTCTGGAAAGAAACAAACAGCCAAAAATGCCATGTGATTTGACTGTGGAATC 540

QY 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db 541 CATGCCAGAGAAATGGAATCTCCCTGCTTTCTGCTTTGTGGTTTCATAGGCCATATAACTGAA 600

QY 197 ----- 197
Db 601 TACTACGGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATG 660

QY 198 -----AsnArgMetTrpArgLys 203
Db 661 CCAGTGGTTAATGTGGATGGTTATGACTACTCATCGAAAAAAGAAATCGAATGTGGAGAAAG 720

QY 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 721 AACCGTTCTTTCTATGCGAACAACTCGTTGTCATCGAACAGACCTTGAACAGAGAACTTCGG 780

QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243
Db 781 TCCAAACACTGCTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGAAAACTTACTGTGGA 840

QY 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIle 263
Db 841 CTTTATCTCTGAGTCAGAACCCAGAACGCGGTGGCTAATTTCTTCTGAGAAGAAATATC 900

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264	Qy	AsnGlnIleLysAlaTyrlleSerMetHisSerTyrSerGlnHisIleValPheProTyr	293
901	Db	AACCACATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATCGTGTTCATAT	960
284	Qy	SerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAla	303
961	Db	TCCTATACTCGAAGCAAAAGCAAAAGACCACGAGGAATTGTCTCTAGTAGCCAGTGAAGCA	1020
304	Qy	ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu	323
1021	Db	GTTCTGGTGCTATTGAGAAACCCGATAAAATATCAGGTATACATGCGCGTGCTCAGAA	1080
324	Qy	ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr	343
1081	Db	ACCTTATACCTAGCTCCTCGAGGTGCGGACGATTGGATCTATGATTTGGGCATCAATAT	1140
344	Qy	SerPhe-----	346
1141	Db	TCGTTTTCAATTGAACCTCGAGATACGGGCAATACGGATCTTGTGCTGAGCGGTTAC	1200
346	Qy	rSerAsnProValGluLysLeuLeuProLeuSerLeuLys	360
1201	Db	ATTAAACCCACTGTGTAAGACGCTTTTGGCGTGTCTCTATAAA	1243

## RESULT.7

US-10-115-479-63

Sequence 63, Application US/10115479  
Publication No. US2004006205A1

GENERAL INFORMATION:

APPLICANT: Li, Li

APPLICANT: Gerlach, Valerie L.

APPLICANT: Liu, Xiaohong

APPLICANT: Miller, Charles E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Zerhusen, Bryan D.

APPLICANT: Pena, Carol E.A.

APPLICANT: Shenoy, Sureesh G.

APPLICANT: Zhong, Haihong

APPLICANT: Smithson, Glendda

APPLICANT: Casman, Stacie J.

APPLICANT: Boldog, Ferenc L.;

APPLICANT: Voss, Edward

APPLICANT: Vernet, Corine

APPLICANT: MacDougall, John A.

APPLICANT: Raetelli, Luca

APPLICANT: Anderson, David W.

APPLICANT: Zhong, Mei

APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.

APPLICANT: Malyanker, Uriel M.

APPLICANT: Shimkets, Richard A.

APPLICANT: Taupier, Raymond J.

APPLICANT: Edinger, Shlomit R.

APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-322 B (Cura 622 PT)

CURRENT APPLICATION NUMBER: US/10/115,479

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 60/281,136

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 60/281,863

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/281,906

PRIOR FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/282,934

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: 60/283,657

PRIOR FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 60/283,678

PRIOR FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: 60/283,687

Db 571 ----- 571  
 Qy 241 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 260  
 Db 572 ---TGTCGACTTTATCTCTGAGTCAGAACCCAGAGTGAAGGCGAGTGGCTAGTTCTTGAGA 628  
 Qy 261 ArgAsnIleAsnGlnIleGlyAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280  
 Db 629 AGAAATATCAACAGATTAAAGCATACATCAGCATGCATTTCATCTCCAGCATATAGTG 688  
 Qy 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 300  
 Db 689 TTTTCATATTCTATACAGAGTAAAGCAAGCAATGAGAACTGCTCTAGTAGCC 748  
 Qy 301 SerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320  
 Db 749 AGTGAAGCAGTTCGTGCTATTGAGAAAATTAGTAAAAATACAGGTATACATGGCCAT 808  
 Qy 321 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 340  
 Db 809 GGCTCAGAAACCTTATACCTAGCTCCTCGAGGTGGGAGCATTTGGATCTATGATTGGGC 868  
 Qy 341 IleLysTyrSerPhe----- 345  
 Db 869 ATCAATATTCGTTTTTCAATTAAGTTCGAGATCGGGCAGCATACGGATTCTTGTGCGG 928  
 Qy 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
 Db 929 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGTGTCTCTAAAA 980

RESULT 8

US-10-115-479-65  
 ; Sequence 65, Application US/10115479  
 ; Publication No. US2004006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Huihong  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Malvanker, Uriel M.  
 ; APPLICANT: Shinkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shalomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
 ; CURRENT APPLICATION NUMBER: US/10/115,479  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,687  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; PRIOR APPLICATION NUMBER: 60/285,325  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SEQ ID NO 65  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (41)..(1103)  
 ; US-10-115-479-65  
 Alignment Scores:  
 Pred. No.: 1,27e-162 Length: 1132  
 Score: 1393.50 Matches: 283  
 Percent Similarity: 67.38% Conservative: 0  
 Best Local Similarity: 67.38% Mismatches: 3  
 Query Match: 72.92% Indels: 134  
 DB: 16 Gaps: 4

US-09-980-881A-2 (1-360) x US-10-115-479-65 (1-1132)  
 Qy 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20  
 Db 41 ATGAAGCTTTGCAGCCTTGCAGTCTCTGTACCCATTGTTCTCTCTGTGAGCAGCATGTC 100  
 Qy 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40  
 Db 101 TTCGCGTTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAA 160  
 Qy 41 ValLeuGlnHisLeuThrThrThrThrGluIleValLeuTrpGlnProValThrAlaAsp 60  
 Db 161 GTTCTACAGATCTTACTACAAATATGAGATTGTTCTCTGGCAGCCGTTAACAGCTGAC 220  
 Qy 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80  
 Db 221 CTTATTGTGAAGAAAAAACAAGTCCATTTTGTAAATGATCTGTATGTCGACATGTG 280  
 Qy 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100  
 Db 281 AAAGCCCATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGGCAGACGTTGGAAGAT 340  
 Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120  
 Db 341 CTTATTCAACAGCAGATTTCCACGACACAGTACGCCCCGAGCTCTCCGCACTGCTACTAT 400  
 Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140  
 Db 401 GAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGATTTATAAATGAGAGGCAT 460  
 Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160  
 Db 461 CCTGATATGCTTACAAAAATCCACATTTGGATCTCTCAATTTGAGAAAGTACCCACTCTATGT 520  
 Qy 161 LeuLys-----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrp 175  
 Db 521 TTAAGGGGTTTCTTTGAGCAGGTTTCTGGAAGAAACAGCAGCCAAATATGCCATATGG 580  
 Qy 176 IleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle 195

581 ATTGACTGTGGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTGTGTTGTTTCATA 640  
QY 196 GlyHis----- 197  
DB 641 GCCCATATAACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTTGTG 700  
QY 198 -----Asn 198  
DB 701 GATTTCTATGTTATGCCGGTGGTTAATGTGGATGGTTATGACTACTCATGGAAGAAGAT 760  
QY 199 ArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeu 218  
DB 761 CGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACCAATCAATTGCAATCGGAACAGACCTG 820  
QY 219 AnnSerAsnPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSer 238  
DB 821 AATAGGAACCTTTGCTTCCAAACACATGTTGTGAGGAGGTGCATCCATGCTCTGCTCG 880  
QY 239 GluThrTyrCysGlyLeuTyrProGluSerGluProGluValysAlaValAlaSerPhe 258  
DB 881 GAAACCTACTGTGGACTTTATCTCTGAG----- 907  
QY 259 LeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHis 278  
DB 907 ----- 907  
QY 279 IleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeu 298  
DB 907 ----- 907  
QY 299 ValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHis 318  
DB 907 ----- 907  
QY 319 GlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAsp 338  
DB 908 -----TCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGAT 958  
QY 339 LeuGlyIleLysTyrSerPhe----- 345  
DB 959 TTGGGCATCAATATTTCTGTTTACAATTGAACCTTCGAGATACGGGCAATACGGATTCTTTG 1018  
QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
DB 1019 CTCCCGAGCGTTACATCAAAACCCACTGTAGAGAAGCTTTTGGCCGCTGTCTCTAATA 1076

RESULT 9

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:

Pred. No.: 1.06e-99 Length: 1400  
Score: 889.00 Matches: 178  
Percent Similarity: 75.21% Conservative: 1  
Best Local Similarity: 74.79% Mismatches: 3  
Query Match: 46.52% Indels: 56  
DB: 9 Gaps: 2  
US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)  
QY 179 GlyIleHisAlaAaGluTyrIleSerProAlaPheCysLeuTyrPheIleGlyHis--- 197  
DB 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGCTGTGTTGTTTCATAGGCCATATA 69  
QY 197 ----- 197  
DB 70 ACTCAATCTATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTTGTGGATTCTAT 129  
QY 198 -----AsnArgMetTr 201  
DB 130 GTTATGCCGGTGGTTAATGTGGATGGTTATGAACCTACTCATGGAAGAAAGATCGAATGTG 189  
QY 201 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAs 221  
DB 190 GAGAAAGAACCGTTCTTCTATGCGAACCAATCAATTGCAATCGGAACAGACCTGAATAGGAA 249  
QY 221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 241  
DB 250 CTTTCTCTCCAAACACTGTTGTGAGGAAGGTGCATCCAGTTCTCATGCTCGGAACCTA 309  
QY 241 cCysGlyLeuTyrProGluSerGluProGluValysAlaValAlaSerPheLeuArgAr 261  
DB 310 CTGTGGACTTTATCTCTGAGTCAGAACCCAGAGAGTGAAGGCAGTGGCTAGTTCTTGAGAAG 369  
QY 261 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 281  
DB 370 AAATATCAACCGAGTTAAAGCATACATCAGCATGATTCATCTACTCCAGCATATAGTGT 429  
QY 281 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 301  
DB 430 TCCATATCTCTATACACGAAGTAAAGCAACACCATGAGGAACCTGTCTCTAGTAGCCAG 489  
QY 301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 321  
DB 490 TGAAGCAGTTCGTGCTATTGAGAAAACCTAGTAAAAATACCAAGGTATACACATGGCCATGG 549  
QY 321 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyI 341  
DB 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609  
QY 341 eLysTyrSerPhe----- 345  
DB 610 CAATATCTGTTTACAAATTGAACCTTCGAGATACGGSCACATACGGATTCTTGTGCGCGA 669  
QY 346 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 360  
DB 670 GCGTTACATCAAAACCCACTGTAGAGAAGCTTTTGGCCGCTGTCTCTAATAA 719  
RESULT 10  
US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24
```

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Alignment Scores:
Pred. No.:      1,06e-99      Length:      1400
Score:          889.00      Matches:      178
Percent Similarity: 75.21%      Conservative: 1
Best Local Similarity: 74.79%      Mismatches: 3
Query Match:      46.52%      Indels:      56
DB:              10          Gaps:      2
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US-09-980-881A-2 (1-360) x US-09-925-302-24 (1-1400)

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Qy 179 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 197
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTCTGTTGTTTCATAGGCCATATA 69
Qy 197 ----- 197
Db 70 ACTCAATTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCAT 129
Qy 198 -----AsnArgMetTr 201
Db 130 GTTATGCCGGTGTAAATGTGGATGGTTATGNACTACTCATGCGAAAAGAAATCGAATGTG 189
Qy 201 pArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnSerAs 221
Db 190 GAGAAAGAACCGTTCTTCTATGCGAACAAATCATTTGCATCGGAACAGACCTGAATAGGAA 249
Qy 221 nPheValSerLysHisTrpCysGluGluGlyAlaSerSerSerSerSerGluThrTy 241
Db 250 CTTTTCGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATCTCGGAACCTA 309
Qy 241 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 261
Db 310 CTGTGGACTTATCTCTGAGTCAGAACCAAGAGTGAAGGCAGTGGTAGTCTTCTTGAGAG 369
Qy 261 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValph 281
Db 370 AAATATCAACACAGATTAAGCATATACATCAGCATGCAATTCATACCTCCAGCATATAGTGT 429
Qy 281 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 301
Db 430 TCCATATTCCCTATACCAAGATTAAGCAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAG 489
Qy 301 rGluAlaValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisG1 321
Db 490 TGAACAGTTCGTGTCTATTGAGAAAACCTAGTAAATAATACCAGGTATACATGCGCATGG 549
Qy 321 ySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyI1 341
Db 550 CTCAGAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609
Qy 341 elyTyrSerPhe----- 345
Db 610 CAATATTCTGTTTCAATTGAACTTCGAGATACGGGCACATACGGATTCTTGTCTCCCGGA 669
Qy 346 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 670 GCGTTACATCAAAACCCACTGCTAGAGAGAGCTTTCCCGCTCTCTAAA 719
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## RESULT 11

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US-09-910-059-124
; Sequence 124, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
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; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised pre-pro HCPB-linker-Fd sequence
US-09-910-059-124
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Alignment Scores:
Pred. No.:      2,7e-66      Length:      2154
Score:          623.00      Matches:      132
Percent Similarity: 53.40%      Conservative: 72
Best Local Similarity: 34.55%      Mismatches: 134
Query Match:      32.60%      Indels:      44
DB:              9          Gaps:      7
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US-09-980-881A-2 (1-360) x US-09-910-059-124 (1-2154)

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Qy 3 LeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
Db 1 ATGTTGGACACTCTGGTTCGTGCTGCTGGCCCTGGCATCTGCTCATCTCATGGTGGTGAG 60
Qy 23 ---PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnVal 41
Db 61 CACTTTGAAGCGGAGAGGTGTTCCGTTTAACCTTGAAGATGAATAACATCACTAAACATA 120
Qy 42 LeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61
Db 121 ATCCGCGAGTTGGCAGCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTCAACAA 180
Qy 62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81
Db 181 ATCAAACTCACATGACAGTTGACTTCGCTGTTAAAGCAGAAAGATCTGTCTACTGTGGAG 240
Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValIgluAspLeu 101
Db 241 AATGTTCTTAAGCAGAGTGAAGTACTACATAAGGTACTGATAAGCAACCTCAGAAATGTG 300
Qy 102 IleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
Db 301 GTGAGGCTCAGTTTGATAGCCGGTT-----CGTGCACAGGACACACAGATTATGAG 351
Qy 122 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141
Db 352 AAGTACAAACAGTGGGAAACGATAGAGCTTGGACTCAACAAAGTCGCCACTGAGAAATCCA 411
Qy 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
Db 412 GCCCTCATCTCTCCAGTGTATTATCGGAACACACATTTGAGGGACCGCGCTATTATCTCTG 471
Qy 162 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 181
Db 472 AAGGTT---GGCAAGGTGGACAAAATAAGCCTGCCATTTTCATGGACTGTGGTTTCCAT 528
Qy 182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
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; PRIORITY FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1141
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1141

Alignment Scores:
Pred. No.: 1,868-66 Length: 1332
Score: 621.50 Matches: 134
Percent Similarity: 53.66% Conservative: 71
Best Local Similarity: 35.08% Mismatches: 132
Query Match: 32.52% Indels: 45
DB: 9 Gaps: 8

US-09-980-881A-2 (1-360) x US-09-954-456-1141 (1-1332)

QY 3 LeuCySerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla 22
DB 24 ATGTTGGCACCTCTGTTCTGGTACATGTGGCCCTGGCATCTGCTCATCATGTGTGTGAG 83
QY 23 ---PheGlnSerGlyGlnValLeuAlaLeuProAthrSerArgGlnValGlnVal 41
DB 84 CACTTTGAAGCGCGAGAGGTGTTCCGTGTTAACTGTTGAAGATGAAAAATCACATTAAACA 143
QY 42 LeuGlnAenLeuThrThrThrGluIleValLeuTyrGlnProValThrAlaLeu 61
DB 144 ATCCCGAGTGTGGCCAGCAGCCAGCATTTGACTTCTGGAGCCAGATTTCTGTCAACA 203
QY 62 IleValLysLysGlnValHisPheValAenAlaSerAspValAspValLys 81
DB 204 ATCAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAGATCTGTCACTGTGGAG 263
QY 82 AlaHisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
DB 264 AATGTTCTAAAGCAGAACTGAATACATACAGAGTACTGATAGCAACCTGAGAAATGTG 323
QY 102 IleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 121
DB 324 GTGGAGGCTCAGTTTGTAGTCCGGGT-----CGTGCACACAGGACACAGATTATGAG 374
QY 122 GlnTyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 141
DB 375 AAGTACACAACTGGGAAACGATAGAGGCTTGAGCTCAACAAGTCGCCACTGAGAAATCCA 434
QY 142 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 161
DB 435 GCCCTCATCTCTCGCAGTGTATTCGGAACACATTTGAGGAGCGCGCTATTTACCTCTCTG 494
QY 162 LysValSerGlyLysGluGlnThrAlaLysAenAlaIleTrpIleAspCysGlyIleHis 181
DB 495 AAGGTT---GGCAAGCTGGACAAATAAGCCCTGCCATTTTCATGGACTGTGGTTCCAT 551
QY 182 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
DB 552 GCCAGAGTGGATTTCTCTGATTTCTCCAGTGTGTTGTAAGAGAGGCTGTTCGTACC 611
QY 195 ----- 195
DB 612 TATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAGTTAGACTTTTATGTCCTGCCT 671
QY 196 -----GlyHis-----AsnArgMetTrpArgLysAen 204
DB 672 GTGCTCAATATTGATGGCTACATCTACCTGACCAAGAGCGGATTTTGGAGAAAGACT 731
QY 205 ArgSerPheTyrAlaAenAenHisCysIleGlyThrAspLeuAenSerAenPheValSer 224
DB 732 CGCTCCACCCTACTGGATCT---AGCATTTGGCAGACAGCCCAACAGAAATTTT---GAT 785
QY 225 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 244
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529 GCCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTGTAAGAGAGGCTGTTGCTACC 588
195 ----- 195
589 TATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAGTTAGACTTTTATGCTCTGCT 648
196 -----GlyHis-----AsnArgMetTrpArgLysAen 204
649 GTGCTCAATATTGATGGCTACATCTACACTGGACCAAGAGCGGATTTTGGAGAAAGACT 708
205 ArgSerPheTyrAlaAenAenHisCysIleGlyThrAspLeuAenSerAenPheValSer 224
709 CGCTCCACCCTACTGGATCTGCTGCAATTCGCCAGAGCTTCTCGACAGAAATTTT---GAT 765
225 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 244
766 GCTGTTGGTGTGAATTTGGAGCTTCTCGAAACCCCTGTGATGAAACTTTACTGTGAGCT 825
245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAenIleAen 264
826 GCGCAGAGTGTGAAGAGAGCAAGGCCCTGGCTGATTTTATCCGCAACAACTCTCT 885
265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284
886 TCCATCAAGCATATCTGACATCTGACTGCTACTCCCAATGATGATCTACCTTACTCA 945
285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
946 TATGCTTACAACTCGGTGAGAACATGCTGAGTTGATGCTCCCTGCTAAAGTACTGTGTG 1005
305 ArgAlaIleAspLysThrSerLysAenThrArgTyrThrHisGlyHisGlySerGluThr 324
1006 AAGAAACTT---GCCTCCTGACGCGCAGCAGATGATGATGATGATGATGATGATGATGAT 1062
325 LeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344
1063 ATCTATCTCTCTGCTGGACTTCTAAAGACTGGCTTATGACCAAGGAATCAGATATTC 1122
345 PheThr 346
1123 TTCACC 1128

RESULT 12
US-09-954-456-1141
; Sequence 1141, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Sets
; FILE REFERENCES: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
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Db 786 CTTGGTGGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAACTTACTTGTGGACCT 845
Qy 245 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsn 264
Db 846 GCCGAGAGTCTGAAAGAGACCAAGCCCTGGCTGATTTTCATCCGCAACAACTCTCT 905
Qy 265 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 284
Db 906 TCCATCAAGGCATATCTGACAACTCCACTCGCTACTCCCAATGATGATCTACCTTACTCA 965
Qy 285 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 304
Db 966 TATGCTTACAACCTCGGTGAGAACATGCTGAGTTGATGCTGGCTGCTAAAGCTACTGTG 1025
Qy 305 ArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 324
Db 1026 AAGAAGCTT---GCTCACTCGCGGACCAAGTACACATATGCGCGGAGCTACAACA 1082
Qy 325 LeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 344
Db 1083 ATCTATCTGCTGTGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTC 1142
Qy 345 PheThr 346
Db 1143 TTCACC 1148

RESULT 13
US-10-341-434-187
; Sequence 187, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 90 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341.434
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 187
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(1262)
; OTHER INFORMATION:
US-10-341-434-187

Alignment Scores:
Pred. No.: 3,48e-66 Length: 1633
Score: 620.50 Matches: 130
Percent Similarity: 54.19% Conservatives: 77
Best Local Similarity: 34.03% Mismatches: 128
Query Match: 32.47% Indels: 47
DB: 15 Gaps: 8

US-09-980-881a-2 (1-360) x US-10-341-434-187 (1-1633)
Qy 5 SerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisValPheAla----- 22
Db 9 ACCATGAGCTCATCTGCTGCTGGTTGATGCTTGTACCACTCTTGTCAATTTGCTCCTGTC 68
Qy 23 ---PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 41
Db 69 CGCTTTGACAGGAGAGAGGTGTCGCGTGAGCCCGAGGATGAAACACAGACAGATC 128
Qy 42 LeuGlnAsnLeuThrThrThrTyrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 61
Db 129 ATAAAGGACTTGGCCAAACCAATGAGCTTGTGATCTTGTGATCTCAGGTGCCACCCACCAC 188
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Qy 62 IleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLys 81
Db 189 GTAGCTCTAATATGATGGTGGATTTCCGAGTTAGTGAGAGGATCCCAAGCAGCTCCAG 248
Qy 82 AlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 101
Db 249 TCTGCTTGGATCAAATAAATGACATATGCAATCTTGATCATGATCTACAGAAGAG 308
Qy 102 IleGlnGlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 309 ATTGAGAAACAGTTGATGTTAAAGAGATATCCAGCGAGGCACAGC-----TAC 359
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 360 GCAAAATACAAATAATGGGAAAAGATGTGGCTTGGACTGAAAGATGATGATTAAGTAT 419
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 420 CTTGAAATGGTCTCTGATTTAAATTTGGATCTACTCTTGAAGATATCCACTATATGTT 479
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 480 CTGAAGATT---GGGGAAGAAATGAAAGAAAGAGCTATTTTATGGATTGTGGCATT 536
Qy 181 HisAlaArgGlnTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 537 CAGCAGAGATGGGTCTCCCGAGCATTTGCCAGTGTGTTGTCTATCAGGCAACAAA 596
Qy 195 ----- 195
Db 597 ACTTATGGGAGAAACAAAATTTATGACCAAACTCTTGACCGAATGAATTTTACATCTT 656
Qy 196 -----GlyHis-----AsnArgMetTrpArgLys 203
Db 657 CTTGTGTTCAATGTTGATGGATATATTTGTCATGGACAAAGAACCGCATGTGGAGAAA 716
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 717 AATCGTTTCCAAGAACCAAAACTCCAAATGTCATGGCACTGACCTCAACAGGAATTTT--- 773
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243
Db 774 AATGCTTCATGGAACTCCATCTCTTAACACCAATGACCCATGTGCAGATACTATCGGGC 833
Qy 244 LeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIle 263
Db 834 TCTGCACAGAGTCCGAGAAAGAGACGAAAGCTGTCTAATAATTTTATTAGAACCACTG 893
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
Db 894 AATGAAATCAAGGTTTATACATCACCTTCCATCTCTTCTCCAGATGCTATTGTTTCCCTAT 953
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303
Db 954 GGATATACATCAAAACTGCCACCTAACCATGAGAGCTTGGCCAAAGTTGCAAGATTGGC 1013
Qy 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
Db 1014 ACTGATGTTCTA---TCAACTCGATATGAAACCGCTACATCTATGTCGCCCAATAGAAATCA 1070
Qy 324 ThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
Db 1071 ACAATTTACCGATATCAGGTCTCTTCTTATAGCTGGGCTTATGACCTGGGATCAAAAC 1130
Qy 344 SerPhe 345
Db 1131 ACATTT 1136

RESULT 14
US-10-116-802-95
; Sequence 95, Application US/10116802
; Publication No. US20030065157A1
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 01:31:47 ; Search time 18.2606 Seconds  
(without alignments)  
1227.533 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 338  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYSPTSNPPVEKLPLSLK 338

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/1aa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB.pep.\*  
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4: /cgn2\_6/prodata/1/1aa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/ECTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	55.0	386	US-09-813-133A-2	Sequence 2, Appli
2	175	51.8	423	US-07-649-591B-3	Sequence 3, Appli
3	175	51.8	423	US-08-277-540-3	Sequence 3, Appli
4	175	51.8	423	US-08-430-787A-3	Sequence 3, Appli
5	175	51.8	423	US-08-869-057-2	Sequence 2, Appli
6	146	43.2	423	US-09-813-133A-4	Sequence 4, Appli
7	31	9.2	37	US-07-649-591B-1	Sequence 1, Appli
8	31	9.2	37	US-08-277-540-1	Sequence 1, Appli
9	31	9.2	37	US-08-430-787A-1	Sequence 1, Appli
10	15	4.4	417	US-07-649-591B-7	Sequence 7, Appli
11	15	4.4	417	US-08-277-540-7	Sequence 7, Appli
12	15	4.4	417	US-08-430-787A-7	Sequence 7, Appli
13	12	3.6	247	US-09-675-305-6	Sequence 6, Appli
14	12	3.6	247	US-10-200-344-6	Sequence 6, Appli
15	12	3.6	350	US-09-675-305-12	Sequence 12, Appli
16	12	3.6	350	US-10-200-344-12	Sequence 12, Appli
17	12	3.6	437	US-09-675-305-10	Sequence 10, Appli
18	12	3.6	437	US-10-200-344-10	Sequence 10, Appli
19	11	3.3	86	US-09-270-767-56648	Sequence 56648, A
20	11	3.3	89	US-09-513-999C-7648	Sequence 7648, Ap
21	11	3.3	216	US-08-270-767-41427	Sequence 41427, A
22	11	3.3	307	US-08-782-760-6	Sequence 6, Appli
23	11	3.3	307	PCT-US96-00995-6	Sequence 6, Appli
24	11	3.3	329	US-09-011-769A-51	Sequence 51, Appli
25	11	3.3	349	US-09-011-769A-47	Sequence 47, Appli
26	11	3.3	349	US-09-011-769A-60	Sequence 60, Appli
27	11	3.3	349	US-09-011-769A-64	Sequence 64, Appli

28	11	3.3	396	1	US-07-649-591B-4	Sequence 4, Appli
29	11	3.3	396	1	US-08-277-540-4	Sequence 4, Appli
30	11	3.3	396	1	US-08-430-787A-4	Sequence 4, Appli
31	11	3.3	415	2	US-08-860-882A-57	Sequence 57, Appli
32	11	3.3	415	4	US-09-011-769A-39	Sequence 39, Appli
33	11	3.3	424	4	US-09-011-769A-56	Sequence 56, Appli
34	11	3.3	613	3	US-09-171-945-113	Sequence 113, App
35	11	3.3	716	3	US-09-171-945-125	Sequence 125, App
36	10	3.0	417	1	US-07-649-591B-6	Sequence 6, Appli
37	10	3.0	417	1	US-08-277-540-6	Sequence 6, Appli
38	10	3.0	417	1	US-08-430-787A-6	Sequence 6, Appli
39	10	3.0	417	4	US-09-517-254-66	Sequence 66, Appli
40	9	2.7	162	4	US-09-248-796A-14973	Sequence 14973, A
41	9	2.7	417	1	US-07-649-591B-8	Sequence 8, Appli
42	9	2.7	417	1	US-08-277-540-8	Sequence 8, Appli
43	9	2.7	417	1	US-08-430-787A-8	Sequence 8, Appli
44	8	2.4	282	3	US-09-412-102-2	Sequence 2, Appli
45	8	2.4	282	3	US-09-217-787-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match	55.0%	Score 186;	DB 4;	Length 386;
Best Local Similarity	99.7%	Pred. No. 1.8e-175;		
Matches	286;	Conservative	0;	Mismatches 1;
Indels	0;	Gaps	0;	
QY	1	FQSGQVLAALPRTSRQVQLNLT	TTT	YI
DB	23	FQSGQVLAALPRTSRQVQLNLT	TTT	YI
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DB	83	HLNVSIGPCSVLLADVEDLI	QOO	I
QY	121	MLTKIHIGSSPKYPLYVLK	VS	KG
DB	143	MLTKIHIGSSPKYPLYVLK	VS	KG
QY	181	KNRSFYANNHCITGDLNR	NF	AS
DB	203	KNRSFYANNHCITGDLNR	NF	AS
QY	241	INQIKAYISMHSYQHI	VP	YS
DB	263	INQIKAYISMHSYQHI	VP	YS

RESULT 2  
US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:

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; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-649-591B-3

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Query Match 51.8%; Score 175; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTDLVKKQVHFFVNASDNDVKA 60
Db 23 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTDLVKKQVHFFVNASDNDVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKYPYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 175
Db 143 MLTKIHGSSFEKYPYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 197

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RESULT 3
US-07-277-540-3
; Sequence 3, Application US/08277540
; Patent No. 547901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 547901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-277-540-3

Query Match 51.8%; Score 175; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.5e-164;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTDLVKKQVHFFVNASDNDVKA 60
Db 23 FQSQVLAALPRTSRQVQLQNLTTTVEIYLWQPVTDLVKKQVHFFVNASDNDVKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKYPYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 175
Db 143 MLTKIHGSSFEKYPYLVKVSKEQTAKNAIWDGCIHAREWISPAFCLWFIGH 197

RESULT 4
US-08-430-787A-3
; Sequence 3, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994

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APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-3

Query Match 51.8%; Score 175; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.5e-164;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKPYLYVLKVSKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 175  
DB 143 MLTKIHIGSSFEPKPYLYVLKVSKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 197

RESULT 5  
US-08-869-057-2  
Sequence 2, Application US/08869057  
Patent No. 5985562  
GENERAL INFORMATION:  
APPLICANT: Morser, Michael J  
APPLICANT: Nagashima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
TISSUE TYPE: Plasma  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 23..401  
US-08-869-057-2

Query Match 51.8%; Score 175; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.5e-164;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKPYLYVLKVSKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 175  
DB 143 MLTKIHIGSSFEPKPYLYVLKVSKEQTAKNAIWDGCIHAREWISPAFLCWFIGH 197

RESULT 6  
US-09-813-133A-4  
Sequence 4, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinu et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CLO01173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 423  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-4

Query Match 43.2%; Score 146; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 6.7e-136;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 60  
DB 23 FOSGQVLAALPRTSRQVQLQNLTTTTEIYVLWQPVTTADLIIVKKQVHFFVNASDVNDVKA 82  
QY 61 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 120  
DB 83 HLNVSIGPCSVLLADVEDLIQQIISNDTVSPRASASYEYQVHSLNEIYSWIEFITERHPD 142  
QY 121 MLTKIHIGSSFEPKPYLYVLKVSKEQ 146  
DB 143 MLTKIHIGSSFEPKPYLYVLKVSKEQ 168

RESULT 7  
US-07-649-591B-1  
Sequence 1, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:

APPLICANT: Dennis Drayna and Daniel Eaton  
 TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/649,591B  
 FILING DATE: 19910201  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/266-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 37 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 US-07-649-591B-1

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Query Match          9.2%; Score 31; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FQSGQVLAALPRTSRQVQLNLTYYEIVL 31  
D6 1 FQSGQVLAALPRTSRQVQLNLTYYEIVL 31

```

RESULT 8
US-08-277-540-1
; Sequence 1, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993

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INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-430-787A-1

Query Match 9.2%; Score 31; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSGQVLAALPRTSRQVQLQLTTTYEIVL 31  
|||||  
Db 1 FQSGQVLAALPRTSRQVQLQLTTTYEIVL 31

RESULT 10  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear

US-07-649-591B-7  
Query Match 4.4%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 DCGIHAREWISPAFC 169  
|||||  
Db 172 DCGIHAREWISPAFC 186  
|||||

RESULT 11  
US-08-277-540-7  
Sequence 7, Application US/08277540  
Patent No. 5474901  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A

TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,540  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/959944  
FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 417 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-277-540-7

Query Match 4.4%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 DCGIHAREWISPAFC 169  
|||||  
Db 172 DCGIHAREWISPAFC 186  
|||||

RESULT 12  
US-08-430-787A-7  
Sequence 7, Application US/08430787A  
Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A

;  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-430-787A-7

Query Match 4.4%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 DCGIHAREWISPAFC 169  
Db 172 DCGIHAREWISPAFC 186

RESULT 13  
US-09-675-305-6  
; Sequence 6, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-675-305-6

Query Match 3.6%; Score 12; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164  
Db 190 WIDCGIHAREWI 201

RESULT 14

US-10-200-344-6  
; Sequence 6, Application US/10200344  
; Patent No. 6780640  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/10/200,344  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-200-344-6

Query Match 3.6%; Score 12; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164  
Db 190 WIDCGIHAREWI 201

RESULT 15  
US-09-675-305-12  
; Sequence 12, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: LEX-0047-USA  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-675-305-12

Query Match 3.6%; Score 12; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164  
Db 190 WIDCGIHAREWI 201

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OM protein - protein search, using sw model

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Title: US-09-980-881A-3  
Perfect score: 338  
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Searched: 1364641 seqs, 323758627 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0  
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  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	55.0	386	9 US-09-813-133A-2	Sequence 2, Appli
2	186	55.0	386	14 US-10-212-877-2	Sequence 2, Appli
3	175	51.8	423	14 US-10-379-836-17	Sequence 17, Appl
4	149	44.1	211	9 US-09-925-302-467	Sequence 467, App
5	149	44.1	211	10 US-09-925-302-467	Sequence 467, App
6	146	43.2	322	15 US-10-115-479-64	Sequence 64, Appl
7	146	43.2	423	9 US-09-813-133A-4	Sequence 4, Appli
8	146	43.2	423	14 US-10-212-877-4	Sequence 66, Appl
9	140	41.4	354	15 US-10-115-479-66	Sequence 68, Appl
10	140	41.4	428	15 US-10-115-479-68	Sequence 70, Appl
11	140	41.4	428	15 US-10-115-479-70	Sequence 2, Appli
12	60	17.8	423	14 US-10-379-836-2	Sequence 18, Appl
13	27	8.0	422	14 US-10-379-836-18	

14	26	7.7	422	14	US-10-379-836-16	Sequence 16, Appl
15	12	3.6	210	16	US-10-363-829-401	Sequence 401, App
16	12	3.6	247	13	US-10-200-344-6	Sequence 6, Appli
17	12	3.6	315	9	US-09-888-615-60	Sequence 60, Appl
18	12	3.6	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	3.6	434	16	US-10-477-515-2	Sequence 2, Appli
20	12	3.6	437	13	US-10-200-344-10	Sequence 10, Appl
21	12	3.6	437	14	US-10-274-639-12	Sequence 12, Appl
22	12	3.6	437	15	US-10-333-574-12	Sequence 128, App
23	12	3.6	437	17	US-10-757-262-128	Sequence 274, App
24	11	3.3	118	15	US-10-074-978A-274	Sequence 48, Appl
25	11	3.3	231	15	US-10-074-978A-48	Sequence 50, Appl
26	11	3.3	231	15	US-10-074-978A-50	Sequence 52, Appl
27	11	3.3	231	15	US-10-074-978A-52	Sequence 46, Appl
28	11	3.3	349	15	US-10-074-978A-46	Sequence 20, Appl
29	11	3.3	402	14	US-10-379-836-20	Sequence 266, App
30	11	3.3	416	15	US-10-074-978A-266	Sequence 267, App
31	11	3.3	417	15	US-10-074-978A-267	Sequence 268, App
32	11	3.3	417	15	US-10-074-978A-268	Sequence 3, Appli
33	11	3.3	417	16	US-10-477-515-3	Sequence 113, App
34	11	3.3	613	9	US-09-910-059-113	Sequence 4, Appli
35	11	3.3	613	16	US-10-608-710-4	Sequence 125, App
36	11	3.3	716	9	US-09-910-059-125	Sequence 6143, Ap
37	10	3.0	180	14	US-10-106-698-6143	Sequence 54, Appl
38	10	3.0	231	15	US-10-074-978A-54	Sequence 1959, Ap
39	10	3.0	286	16	US-10-408-765A-1959	Sequence 20, Appl
40	10	3.0	310	16	US-10-470-390A-20	Sequence 61, Appl
41	10	3.0	374	9	US-09-888-615-61	Sequence 270, App
42	10	3.0	416	15	US-10-074-978A-270	Sequence 2, Appli
43	10	3.0	417	14	US-10-229-546-2	Sequence 9, Appli
44	10	3.0	417	14	US-10-229-546-9	Sequence 188, App
45	10	3.0	417	14	US-10-341-434-188	

ALIGNMENTS

RESULT 1  
US-09-813-133A-2  
; Sequence 2, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 386  
; TYPE: PRT  
; ORGANISM: Human  
US-09-813-133A-2

Query Match 55.0%; Score 186; DB 9; Length 386;  
Best Local Similarity 99.7%; Pred. No. 5.1e-171;  
Matches 286; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	FOSGQVLAALPRTSRQVQLQTLTTTYYEIVLWPQTADLIIVKKQVHFFVNASDVNVKA	60
Db	23	FOSGQVLAALPRTSRQVQLQTLTTTYYEIVLWPQTADLIIVKKQVHFFVNASDVNVKA	82
Qy	61	HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYRQYHSLNIYSWIEFITERHPD	120
Db	83	HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYRQYHSLNIYSWIEFITERHPD	142
Qy	121	MLTKIHIGSFEPKYPYLVKVSKEQTAKNAIWDGHIHAREWISPAFCIWPFIHNRMR	180
Db	143	MLTKIHIGSFEPKYPYLVKVSKEQTAKNAIWDGHIHAREWISPAFCIWPFIHNRMR	202



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; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467

Query Match      44.1%; Score 149; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.8e-135;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 NRMWRKRSFYANNHCIGTDLNRFASKWCEGASSSSCSSTCYCGLYPESEPEVKAVAS 235
    |||||||
DB 23 NRMWRKRSFYANNHCIGTDLNRFASKWCEGASSSSCSSTCYCGLYPESEPEVKAVAS 82

QY 236 FLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYT 295
    |||||||
DB 83 FLRRNINQIKAYISMHSYSHIVFPYSYTRSKSKOHEELSLVASEAVRAIEKTSKNTRYT 142

QY 296 HGRGSETLYLAPGGDDWIYDLGIKYSFT 324
    |||||||
DB 143 HGRGSETLYLAPGGDDWIYDLGIKYSFT 171

RESULT 6
US-10-115-479-64
; Sequence 64, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerkusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 64
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-64

Query Match      43.2%; Score 146; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOSGOVLAALPRTSRQOVQLNLTTTYEIVLWQPVTADLIVKKQVHFVNASDVNDVKA 60
    |||||||
DB 23 FOSGOVLAALPRTSRQOVQLNLTTTYEIVLWQPVTADLIVKKQVHFVNASDVNDVKA 82

QY 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
    |||||||
DB 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142

QY 121 MLTKIHIGSSFKEKYPLYVLKVSQKEQ 146
    |||||||
DB 143 MLTKIHIGSSFKEKYPLYVLKVSQKEQ 168

RESULT 7
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinui et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-4

Query Match      43.2%; Score 146; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.6e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOSGOVLAALPRTSRQOVQLNLTTTYEIVLWQPVTADLIVKKQVHFVNASDVNDVKA 60
    |||||||
DB 23 FOSGOVLAALPRTSRQOVQLNLTTTYEIVLWQPVTADLIVKKQVHFVNASDVNDVKA 82

QY 61 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 120
    |||||||
DB 83 HLNVSIGIPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIEFITERHPD 142

QY 121 MLTKIHIGSSFKEKYPLYVLKVSQKEQ 146
    |||||||
DB 143 MLTKIHIGSSFKEKYPLYVLKVSQKEQ 168

RESULT 8
US-10-212-877-4
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; Sequence 4, Application US/10212877
; Publication No. US2003001/574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: NUCLEATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: ISOLATED ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Human
US-10-212-877-4

Query Match 43.2%; Score 146; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.6e-132;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNYKA 60
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNYKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYVEQVHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYVEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKYPYLVKVGREQ 146
Db 143 MLTKIHGSSFEKYPYLVKVGREQ 168

RESULT 9
US-10-115-479-66
; Sequence 66, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkers, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
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; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 66
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-66

Query Match 41.4%; Score 140; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNYKA 60
Db 23 FQSGQVLAALPRTSRQVQLQNLTTTVEIVLWQPVTDLIIVKKQVHFFVNASVDVNYKA 82

Qy 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYVEQVHSLNEIYSWIEFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASAYVEQVHSLNEIYSWIEFITERHPD 142

Qy 121 MLTKIHGSSFEKYPYLVK 140
Db 143 MLTKIHGSSFEKYPYLVK 162

RESULT 10
US-10-115-479-68
; Sequence 68, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
```

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; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 68
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-68

Query Match          41.4%; Score 140; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.7e-126; Indels 0; Gaps 0;
Matches 140; Conservative 0; Mismatches 0;

QY 1 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTTADLIIVKKQVHFFVNASDNDVKA 60
Db 23 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTTADLIIVKKQVHFFVNASDNDVKA 82

QY 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 142

QY 121 MLTKIHIGSSFEPKYPYLVK 140
Db 143 MLTKIHIGSSFEPKYPYLVK 162

RESULT 11
US-10-115-479-70
; Sequence 70, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
```

```
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera E.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

Query Match          41.4%; Score 140; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.7e-126; Indels 0; Gaps 0;
Matches 140; Conservative 0; Mismatches 0;

QY 1 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTTADLIIVKKQVHFFVNASDNDVKA 60
Db 23 FOSGOVLAALPRTSRQVQLQNLTTTYEIVLWQPVTTADLIIVKKQVHFFVNASDNDVKA 82

QY 61 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 120
Db 83 HLNVSIGPCSVLLADVEDLIQQQISNDTVSPRASASYEQYHSLNEIYSWIFITERHPD 142

QY 121 MLTKIHIGSSFEPKYPYLVK 140
Db 143 MLTKIHIGSSFEPKYPYLVK 162

RESULT 12
US-10-379-836-2
; Sequence 2, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
```

```

; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-10-379-836-2

Query Match      17.8%; Score 60; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.6e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 SDVNVKALNVSGTIPCSVLADVEDLITQOISNDTVSPRASASYEQYHSLNLIYSWIE 112
Db 75 SDVNVKALNVSGTIPCSVLADVEDLITQOISNDTVSPRASASYEQYHSLNLIYSWIE 134

RESULT 13
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Query Match      8.0%; Score 27; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 NDTVSPRASASYEQYHSLNLIYSWIE 112
Db 107 NDTVSPRASASYEQYHSLNLIYSWIE 133

RESULT 14
US-10-379-836-16
; Sequence 16, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; TITLE OF INVENTION: TAFI
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 16
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-379-836-16

Query Match      7.7%; Score 26; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 149 KNAIWIDCGIHAREWISPAFLWFIG 174
Db 170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 15
US-10-363-829-401
; Sequence 401, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daifo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Ching, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 401
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 102
; OTHER INFORMATION: unknown or other
; US-10-363-829-401

Query Match      3.6%; Score 12; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WIDCGIHAREWI 164
Db 48 WIDCGIHAREWI 59

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Search completed: October 27, 2004, 01:56:33  
Job time : 45.3983 secs

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Db 143 CAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTACACAGCTGACCTTATT 202  
Qy 41 VallyslylsGlnValHisPhePheValAsnAlaSerValAspAsnValLysAla 60  
Db 203 GTGAAGAAAAACAAGTCCATTTTTTTTGTAAATGCATCTGATGTGCAATGTGAAAGCC 262  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
Db 263 CATTTAAATGTGACGGAATTCATGAGTGTCTGTGGCAGATGTGGAAGATCTTATT 322  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTCCAAAGCAGACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 382  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAAATGAATCTATCTTGGATAGATTTTATACTGAGAGGCATCTCGAT 442  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTACAAAAATCCCAATGGATCTCTATTGAGAAGTACCCCACTCTATGTTTTAAAG 502  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAl 160  
Db 503 GTTCTCGAAAGAACACAGC-AGCCAAAATGCCATATGGATTGACTGTGAATCCATGC 561  
Qy 160 aArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpAr 180  
Db 562 CAGAGATGGATCTCTCTGCTTCTGCTGTTGTTTATAGGCCATATCGAATGTGGAG 621  
Qy 180 gLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPh 200  
Db 622 AAAGAACCGTTCCTTCTATGGAACAATCATTTGATCGGAACAGACCTGGAATGAAGACTT 681  
Qy 200 eAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCy 220  
Db 682 TGCTTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTG 741  
Qy 220 sGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAs 240  
Db 742 TGGACTTTATCTCAGTCAGAACAGAGAGTGAAGCAGTGGCTAGTGTCTTGTGAAGAAA 801  
Qy 240 nIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePr 260  
Db 802 TATCAACAGATTAAACATACATCAGCATGCAATCATCTCCAGCATATAGTGTTC 861  
Qy 260 oTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGl 280  
Db 862 ATATTCTATACAGAAAGTAAAGCAAGAACCATGAGGAACTGTCTCTAGTAGCCAGTGA 921  
Qy 280 uAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlyS 300  
Db 922 AGCAGTTCGTGCTATTGAGAAAATT-AGTAAAAATACCAGGTATACATGCGCATGGCT 980  
Qy 300 erGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleL 320  
Db 981 CAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGGATCTATGATTTGGGCATCA 1040  
Qy 320 yTyrSerPheThr 324  
Db 1041 AATATTCGTTTACA 1054

## RESULT 2

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko  
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PUBLICATION INFORMATION:  
AUTHORS: Eaton, Dan L.  
AUTHORS: Malloy, Beth E.  
AUTHORS: Tsai, Siao P.  
AUTHORS: Henzel, William  
AUTHORS: Drayna, Dennis  
TITLE: Isolation, Molecular Cloning, and Partial  
TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
TITLE: from Human Plasma  
JOURNAL: J. Biol. Chem.  
VOLUME: 266  
ISSUE: 32  
PAGES: 21833-21838  
DATE: No. 5985562 15-1991  
US-08-869-057-1

## Alignment Scores:

Pred. No.: 1.59e-175 Length: 1272  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 2 Gaps: 0

US-09-980-881A-3 (1-338) x US-08-869-057-1 (1-1272)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 67 TTTTCAGAGTGGCCAAAGTTCTAGTGTCTTCTTAGAACCTCTTAGGCAAGTTCAGATTCTA 126  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuile 40  
Db 127 CAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCGGTACAGCTGACCTTATT 186  
Qy 41 VallyslylsGlnValHisPhePheValAsnAlaSerValAspAsnValLysAla 60  
Db 187 GTGAAGAAAAACAAGTCCATTTTTTTGTAAATGCATCTGATGTGCAATGTGAAAGCC 246  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
Db 247 CATTTAAATGTGACGGAATTCATGAGTGTCTTGTGCGACGCTGGAAGATCTTATT 306  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100

Db 307 CAACAGCAGATTCCAAACAGACACAGCTCAGCCCCCGAGCGCTCGCATCTGCTATGAAACAG 366  
 QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
 Db 367 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGCACTCTGAT 426  
 QY 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
 Db 427 ATGCTTACAAAATCCACATGAGTCTCTATTGAGAAGTACCCACTCTATGTTTAAAG 486  
 QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
 Db 487 GTTCTGGAAAAGAAACAAACAGCCAAAATGCGATATGATGCTGTGAATCCATGCC 546  
 QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
 Db 547 AGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 591

RESULT 3

US-07-649-591B-2  
 ; Sequence 2, Application US/07649591B  
 ; Patent No. 5206161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis Drayna and Daniel Eaton  
 ; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/649,591B  
 ; FILING DATE: 19910201  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.  
 ; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: 689  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/266-1896  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1749 bases  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: hybridization probe  
 ; LOCATION: 133 to 178  
 ; IDENTIFICATION METHOD:  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; NAME/KEY: potential clip site  
 ; LOCATION: 380 to 382  
 ; IDENTIFICATION METHOD:  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; NAME/KEY: signal sequence  
 ; LOCATION: 41 to 106  
 ; IDENTIFICATION METHOD:

OTHER INFORMATION:  
 US-07-649-591B-2  
 Alignment Scores: 2,188-175 Length: 1749  
 Score: 175.00 Matches: 175  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 51.78% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)  
 QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
 Db 107 TTTCCAGAGTGGCCCAAGTTCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCACAGTCTTA 166  
 QY 21 GlnAsnLeuThrThrThrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
 Db 167 CAGAACTTTACTACAAACATATGAGATTCTTCTGGCAGCCGGTAACAGCTGACCTTAAT 226  
 QY 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60  
 Db 227 GTGAGAGAAAAACAAAGTCCATTTTTTTGTAATGCAATCTGATTCGACAAATGTGAAGCC 286  
 QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
 Db 287 CATTTAAATGTGAGCGGAATCCATGCACTGCTTGTGGCAGAGCTGCGAAGATCTTAAT 346  
 QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
 Db 347 CAACAGCAGATTTCACACGACACAGCTCAGCCCCCGAGCTCCGCACTCGTACTATGAACAG 406  
 QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
 Db 407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATTAACCTGAGAGGCACTCTGAT 466  
 QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
 Db 467 ATGCTTACAAAAATCCACATTCATTCCTCATTTGAGAAAGTACCCACTCTATGTTTAAAG 526  
 QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
 Db 527 GTTCTCGAAAAGAAACAAACAGCCAAAATGCCATATGGAATGACTGTGGAATCCATGCC 586  
 QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
 Db 587 AGAGAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCAT 631

RESULT 4

US-08-277-540-2  
 ; Sequence 2, Application US/08277540  
 ; Patent No. 5474901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/277,540  
 ; FILING DATE: 19-JUL-1994  
 ; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/167727  
;; FILING DATE: 15-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/959944  
;; FILING DATE: 14-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/649591  
;; FILING DATE: 01-FEB-91  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hasak, Janet E.  
;; REGISTRATION NUMBER: 28,616  
;; REFERENCE/DOCKET NUMBER: 689D1C1D1  
;; TELEPHONE: 415/225-1896  
;; TELEFAX: 415/952-9881  
;; TELEX: 910/371-7168  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1749 bases  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-277-540-2

Alignment Scores:  
Pred. No.: 2.18e-175 Length: 1749  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCAGAGTGGCCAGTTCTAGTGTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 167 CAGAACTTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226  
Qy 41 VallysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 287 CATTTAAATGTAGCGGAAATTCATGACGTCTTCTGGCAGACGTGGAAGATCTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTTCAACAGCACAGTACAGCCCGAGCCTCCGCATCGTACTATGAACAG 406  
Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCCTCAATGAATCAATCTTCTTGGATAGAAATTTATTAACCTGAGAGCATCCTGAT 466  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAAATCCCATTTGGATTCCTCATTTGAGAAGATACCCACTCTATGTTTAAAG 526  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 527 GTTTCTGAAAGAAACAACAGCCAAATATGCCATATGATGATTGACTGTGGAAATCCATGCC 586  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 587 AGAAGATGGATCTCTCTCGCTTCTTGCTTGTGGTTCATAGGCCAT 631  
RESULT 5  
US-08-430-787A-2

;; Sequence 2, Application US/08430787A  
;; Patent No. 5593674  
;; GENERAL INFORMATION:  
;; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
;; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 460 Point San Bruno Blvd  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: patin (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/430,787A  
;; FILING DATE: 27-APR-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/277,540  
;; FILING DATE: 19-JUL-1994  
;; APPLICATION NUMBER: 08/167727  
;; FILING DATE: 15-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/959944  
;; FILING DATE: 14-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/649591  
;; FILING DATE: 01-FEB-91  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hasak, Janet E.  
;; REGISTRATION NUMBER: 28,616  
;; REFERENCE/DOCKET NUMBER: 689D1C1D1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415/225-1896  
;; TELEX: 910/371-7168  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1749 bases  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 2.18e-175 Length: 1749  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCAGAGTGGCCAGTTCTAGTGTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 167 CAGAACTTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226  
Qy 41 VallysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80



Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 9

US-09-675-305-11

; Sequence 11, Application US/09675305

; Patent No. 6441153

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and

; FILE REFERENCE: Lex-0047-USA

; CURRENT APPLICATION NUMBER: US/09/675,305

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: US 60/156,685

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 1050

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-675-305-11

Alignment Scores:

Pred. No.:	0.00429	Length:	1050
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.55%	Indels:	0
DB:	4	Gaps:	0

US-09-980-881A-3 (1-338) x US-09-675-305-11 (1-1050)

Qy 153 TptleAspCysGlyIleHisAlaArgGluTrpIle 164

Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 10

US-10-200-344-11

; Sequence 11, Application US/10200344

; Patent No. 6780640

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and

; FILE REFERENCE: Lex-0047-USA

; CURRENT APPLICATION NUMBER: US/10/200,344

; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: US/09/675,305

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 1050

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-200-344-11

Alignment Scores:

Pred. No.:	0.00429	Length:	1050
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 3.55% Indels: 0

DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-11 (1-1050)

Qy 153 TptleAspCysGlyIleHisAlaArgGluTrpIle 164

Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 11

US-09-675-305-9

; Sequence 9, Application US/09675305

; Patent No. 6441153

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and

; FILE REFERENCE: Lex-0047-USA

; CURRENT APPLICATION NUMBER: US/09/675,305

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: US 60/156,685

; PRIOR FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 1311

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-675-305-9

Alignment Scores:

Pred. No.:	0.00535	Length:	1311
Score:	12.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.55%	Indels:	0
DB:	4	Gaps:	0

US-09-980-881A-3 (1-338) x US-09-675-305-9 (1-1311)

Qy 153 TptleAspCysGlyIleHisAlaArgGluTrpIle 164

Db 568 TGGATAGACTGGTATTTCATGCAAGAGATGGATT 603

RESULT 12

US-10-200-344-9

; Sequence 9, Application US/10200344

; Patent No. 6780640

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and

; FILE REFERENCE: Lex-0047-USA

; CURRENT APPLICATION NUMBER: US/10/200,344

; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: US/09/675,305

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 1311

; TYPE: DNA

; ORGANISM: homo sapiens

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US-10-200-344-9
Alignment Scores:
Pred. No.: 0.00535 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-9 (1-1311)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 13
US-09-675-305-13
; Sequence 13, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambronicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-13

Alignment Scores:
Pred. No.: 0.00865 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-675-305-13 (1-2128)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 968

RESULT 14
US-10-200-344-13
; Sequence 13, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambronicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
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; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-13

Alignment Scores:
Pred. No.: 0.00865 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.55% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-200-344-13 (1-2128)
Qy 153 TptileAspCysGlyIleHisAlaArgGluTrpIle 164
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 968

RESULT 15
US-09-270-767-25119
; Sequence 25119, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25119
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25119

Alignment Scores:
Pred. No.: 0.0122 Length: 258
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.25% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-270-767-25119 (1-258)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAla 167
Db 127 GGCATCCACGCCCGCAATGGATCAGCCCCCGC 159

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Job time : 111.797 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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-MAXLEN=2000000000 -USER=US0980881@cgn\_1\_1034\_@runat\_26102004\_084213\_7638  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	175	51.8	1728	9	US-09-880-107-2396
4	149	44.1	1400	9	US-09-925-302-24
5	149	44.1	1400	10	US-09-925-302-24
6	146	43.2	1037	16	US-10-115-479-63
7	140	41.4	1132	16	US-10-115-479-65
8	140	41.4	1344	16	US-10-115-479-69
9	140	41.4	1743	16	US-10-115-479-67
10	68	20.1	55827	9	US-09-813-133A-3
11	68	20.1	55827	14	US-10-212-877-3
12	60	17.8	1272	15	US-10-379-836-1
13	43	12.7	1547	13	US-10-027-632-265133
14	43	12.7	1547	13	US-10-027-632-265134
15	43	12.7	1547	13	US-10-027-632-265135
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19	43	12.7	1547	15	US-10-027-632-265135
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21	19	5.6	60	10	US-09-908-975-8511
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28	12	3.6	1050	13	US-10-200-344-11
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33	12	3.6	1907	18	US-10-757-262-127
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36	12	3.6	2128	13	US-10-200-344-13
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39	11	3.3	230	14	US-10-060-036-3096
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44	11	3.3	230	14	US-10-060-036-3168
45	11	3.3	230	14	US-10-060-036-3175

## ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:

Pred. No.: 6.58e-184 Length: 1625  
Score: 186.00 Matches: 322  
Percent Similarity: 98.77% Conservative: 0  
Best Local Similarity: 98.77% Mismatches: 2  
Query Match: 55.03% Indels: 4  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

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Db 83 TTTCCAGAGTGCCAAAGTTCTAGTCTCTCTAGAACCTCTAGCAAGTTCAAGTTCTA 142
Qy 21 GlnAsnLeuThrThrTyrrGluileValLeuTrpGlnProValThrAlaAspLeuile 40
Db 143 CAGAACTCTTACTAACACATATGAGATTGTTCTTGGCAGCCGGTAACAGCTGACCTTAT 202
Qy 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVallyysAla 60
Db 203 GTGAAGAAAAAACAAGTCCATTTTTTGTAAATGCACTGTGATGCGACATGTGAAGCC 262
Qy 61 HisLeuAsnValSerGlyileProCysSerValLeuLeuAlaAspValGluAspLeuile 80
Db 263 CATTTAAATGTGAGCGGAATCCATGCACTGTTCTGGCAGATGTGGAAGATCTTATT 322
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrrGluGln 100
Db 323 CAACAGCAGATTTTCCACGACACAGTACAGCCCGAGCCCTCCGATCGTACTATGAACAG 382
Qy 101 TyrHisSerLeuAsnGluileTyrrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 383 TATCACTCACTAATGAATCTTATCTTGGATAGAAATTTATTAACAGAGCATCTTGAT 442
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrrProLeuTyrrValLeuLys 140
Db 443 ATGCTTACAAAAATCCCAAGTCCATTTTTTGTAAATGCACTGTGATGCGACATGTGAAG 502
Qy 141 ValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAl 160
Db 503 GTTTCTGGAAGAAACAAGC-AGCCAAAAATGCCATATGGATTGACTGTGGAATCCCATGC 561
Qy 160 aArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpAr 180
Db 562 CAGAAATGGATCTCTCTGCTTCTGCTTGTGTTCTATAGCCATATATCGAATGTGGAG 621
Qy 180 gLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPh 200
Db 622 AAAGAACCGTTCTTCTATCGCAACAATCAATTCATCGAACACAGACCTGGAATAGCAACTT 681
Qy 200 eAlaSerLysHisTrpCysGluGluGluValAsrSerSerSerCysSerGluThrTyrrCy 220
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Qy 240 nileAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPhePr 260
Db 802 TATCAACAGATTTAAAGCATATCATCAGCATGCATTCATCTACCTCCAGCATATAGTGTTC 861
Qy 260 oTyrrSerTyrrThrArgSerLysSerLysAspHisGluLuleuSerLeuAlaSerGl 280
Db 862 ATATTCTTATACCAAGTAAAGCAAGACCATGAGGAATGTCTCTAGTAGCCAGTGA 921
Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrrThrHisGlyHisGlys 300
Db 922 AGCAGTTCTGCTATTGAGAAAT-AGTAAAAATACCAAGGTATACATCGCCATGGCT 980
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; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 09/813,133
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1

Alignment Scores:
Pred. No.: 6.58e-184 Length: 1625
Score: 186.00 Matches: 322
Percent Similarity: 98.77% Conservative: 0
Best Local Similarity: 98.77% Mismatches: 2
Query Match: 55.03% Indels: 4
DB: 9 Gaps: 0
US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

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Qy 21 GlnAsnLeuThrThrTyrrGluileValLeuTrpGlnProValThrAlaAspLeuile 40
Db 143 CAGAACTCTTACTAACACATATGAGATTGTTCTTGGCAGCCGGTAACAGCTGACCTTAT 202
Qy 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVallyysAla 60
Db 203 GTGAAGAAAAAACAAGTCCATTTTTTGTAAATGCACTGTGATGCGACATGTGAAGCC 262
Qy 61 HisLeuAsnValSerGlyileProCysSerValLeuLeuAlaAspValGluAspLeuile 80
Db 263 CATTTAAATGTGAGCGGAATCCATGCACTGTGTTCTTGGCAGATGTGGAAGATCTTATT 322
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrrTyrrGluGln 100
Db 323 CAACAGCAGATTTTCCACGACACAGTACAGCCCGAGCCCTCCGATCGTACTATGAACAG 382
Qy 101 TyrHisSerLeuAsnGluileTyrrSerTrpIleGluPheIleThrGluArgHisProAsp 120
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Db 443 ATGCTTACAAAAATCCCAAGTCCATTTTTTGTAAATGCACTGTGATGCGACATGTGAAG 502
Qy 141 ValSerGlyLysGluGlnThr-AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAl 160
Db 503 GTTTCTGGAAGAAACAAGC-AGCCAAAAATGCCATATGGATTGACTGTGGAATCCCATGC 561
Qy 160 aArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpAr 180
Db 562 CAGAAATGGATCTCTCTGCTTCTGCTTGTGTTCTATAGCCATATATCGAATGTGGAG 621
Qy 180 gLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPh 200
Db 622 AAAGAACCGTTCTTCTATCGCAACAATCAATTCATCGAACACAGACCTGGAATAGCAACTT 681
Qy 200 eAlaSerLysHisTrpCysGluGluGluValAsrSerSerSerCysSerGluThrTyrrCy 220
Db 682 TGCCTTCCAAACACATGGTGTGAGGAGGTGCATCCAGTTCCCTCATGCTCGGAACCTACTG 741
Qy 220 sGlyLeuTyrrProGluSerGluProGluVallyysAlaValAlaSerPheLeuArgAs 240
Db 742 TGGACTTTATCTGAGTCAGAACCCAGAAAGTAGGAGCAGTGCTAGTTTCTTGAGAGNAA 801
Qy 240 nileAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGlnHisIleValPhePr 260
Db 802 TATCAACAGATTTAAAGCATATCATCAGCATGCATTCATCTACCTCCAGCATATAGTGTTC 861
Qy 260 oTyrrSerTyrrThrArgSerLysSerLysAspHisGluLuleuSerLeuAlaSerGl 280
Db 862 ATATTCTTATACCAAGTAAAGCAAGACCATGAGGAATGTCTCTAGTAGCCAGTGA 921
Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrrThrHisGlyHisGlys 300
Db 922 AGCAGTTCTGCTATTGAGAAAT-AGTAAAAATACCAAGGTATACATCGCCATGGCT 980
Qy 300 erGluThrLeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrrAspLeuGlyIleL 320
Db 981 CAGAAACCTTATACCTAGCTCTCGAGGTGGGACGATTGGATCTATGATTTGGGCATCA 1040
```

Db 622 AAGAACCGTCTTCTATGCGAACATATGTCATCGGACAGACCTGAAATAGGAACCT 681  
Qy 200 eAlaSerLysHisTrpCysGluGluGlyAlaSerSerCysSerGluThrTyrcy 220  
Db 682 TGCCTCCAAACACTGGTGTGAGAGAGTGCATCCAGATTCTCATGCTCGGAAACCTACTG 741  
Qy 220 sGlyLeuTyProGluSerGluProGluValLysAlaValAlaSerPheLeuAtgAtgAs 240  
Db 742 TGGACTTATCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTCTTCTTGAGAGAAA 801  
Qy 240 nileAsnGlnIleLysAlaTyIleSerMetHisSerTyrsGlnHisIleValPhePr 260  
Db 802 TATCAACAGATTAAAGCATACATCAGCATGCTATCTATCTCCAGCATATAGTGTCTCC 861  
Qy 260 oTyrsTyThrArgSerLysSerLysHisGluGluLeuSerLeuValAlaSerGl 280  
Db 862 ATATTCTCTATACACGAAATGAAAGCAAGACCATGAGGAACCTGTCTCTAGTAGCCAGTGA 921  
Qy 280 uAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyThrHisGlyHisGlyS 300  
Db 922 AGCAGTTCGTGTATTGAGAAATT-AGTAAATAATACAGGTATACACATGSCCATGCGT 980  
Qy 300 exGluThrLeuTyLeuAlaProGlyGlyGlyAspTrpIleTyAspLeuGlyIleL 320  
Db 981 CAGAAACCTTATACCTAGCTCTCGGAGGTGGGACGATTGGATCTATGATTTGGGCATCA 1040  
Qy 320 yTySerPheThr 324  
Db 1041 AATATTCTGTTTACA 1054

RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherif, Uwe  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:  
Pred. No.: 2,12e-172 Length: 1728  
Score: 175.00 Matches: 175  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.78% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTTCAGAGTGGCCAAAGTCTAGCTCTCTCCAGAACCTCTAGGAAGTCAAGTTCTA 145  
Qy 21 GlnAsnLeuThrThrThrTyThrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40

Db 146 CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAACAGCTGACCTTATT 205  
Qy 41 VallysLysGlnValHisPheValAsnAlaSerAspValAspAsnVallyeAla 60  
Db 206 GTGAAGAAAAAACAAAGTCCATTTTTTGTAAATGCACTGATGTCGACAAATGTGAAGCC 265  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 266 CATTTAAATGTAGCGGAATTCATGTCAGTGTCTTGTGGCAGACCTGGAAGATCTTATT 325  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyTyGluGln 100  
Db 326 CAACAGCAGATTTCCAACGACACATGTCAGCCCCCGAGCCTCCGCATCTGATATGAACAG 385  
Qy 101 TyHisSerLeuAsnGluIleTySerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCACTAAATGAATCTATCTTGGATAGATTTATTAACATGAGAGCATCTGAT 445  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyProLeuTyrvValLeuLys 140  
Db 446 ATGCTTACAAAAATCCACATTTGGATCTCTCAITTTGAGAAAGTACCCACTCTATGTTTTAAAG 505  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 506 GTTTCGTGAAAGAAACAAACAGCCAAAAATGCCATATGATGATGACTGTGGAAATCCATGCC 565  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 566 AGAAGATGGATCTCTCTGCTTTTCGTGTTGGTTTCATAGGCCAT 610

RESULT 4

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 2,42e-145 Length: 1400  
Score: 149.00 Matches: 149  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 44.08% Indels: 0  
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy 176 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrApp 195  
Db 179 ATTCGATGTGGAGAAGAACCGTCTTCTATGCGAACAAATCATTCATTCGGAACAGAC 238  
Qy 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 215

Db 239 CTGATAGAACCTTTGCTTCCAAACACCTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 298  
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235  
Db 299 TCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGCCAGTGGCTAGT 358  
Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255  
Db 359 TTCCTTGAGAAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATATCCATCCAG 418  
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275  
Db 419 CATATAGTGTTCATATTCCTATACACGAGTAAAGCAAGACCATGAGGAACTGTCT 478  
Qy 276 LeuValAlaSerGluValAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295  
Db 479 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAATACCAGGTATACA 538  
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 315  
Db 539 CATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 598  
Qy 316 AspLeuGlyIleLysTyrSerPheThr 324  
Db 599 GATTGGGCATCAATATTCGTTTACA 625

## RESULT 5

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

## Alignment Scores:

Pred. No.:	2,42e-145	Length:	1400
Score:	149.00	Matches:	149
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	44.08%	Indels:	0
DB:	10	Gaps:	0

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)

Qy 176 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 195  
Db 179 AATCGAATCTGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTCATCGGAACAGAC 238  
Qy 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 215  
Db 239 CTGATAGAACCTTTGCTTCCAAACACCTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 298  
Qy 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 235  
Db 299 TCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGCCAGTGGCTAGT 358

Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255  
Db 359 TTCCTTGAGAAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATATCCATCCAG 418  
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275  
Db 419 CATATAGTGTTCATATTCCTATACACGAGTAAAGCAAGACCATGAGGAACTGTCT 478  
Qy 276 LeuValAlaSerGluValAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295  
Db 479 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAATACCAGGTATACA 538  
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 315  
Db 539 CATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 598  
Qy 316 AspLeuGlyIleLysTyrSerPheThr 324  
Db 599 GATTGGGCATCAATATTCGTTTACA 625

## RESULT 6

US-10-115-479-63  
; Sequence 63, Application US/10115479  
; Publication No. US20040006205A1

## GENERAL INFORMATION:

; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Perenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13

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; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 2,47e-142 Length: 1037
Score: 146.00 Matches: 146
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.20% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-63 (1-1037)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
DB 107 TTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAspLeu 40
DB 167 CAGAATCTTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226
QY 41 ValLysGlyLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
DB 227 GTGAGAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACCAATGTGAAGCC 286
QY 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80
DB 287 CATTTAAATGTGAGCGGAATTCATGACGTGTTCTTCTGGCAGCGGTAAACAGCTGACCTTATT 346
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
DB 347 CACAGCAGATTTCACACAGACACAGTCAGCCCCGAGCCTCGCATCGTACTATGAACAG 406
QY 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
DB 407 TATCACTCACTAAATGAAATCTATTCTTGATAGAATTTTATACTGAGAGGCATCCTGAT 466
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
DB 467 ATGCTTACAAAAATCCATCGGATCCTCATTTGAGAAAGTACCCTCTATGTTTAAAG 526
QY 141 ValSerGlyLysGluGln 146
DB 527 GTTTCTGGAAGAAAGACAA 544

RESULT 7
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Sytek, Kimberly A.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
```

```
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.: 4,93e-136 Length: 1132
Score: 140.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.42% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
DB 107 TTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrThrTyrGluLeValLeuTrpGlnProValThrAlaAspLeu 40
DB 167 CAGAATCTTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226
QY 41 ValLysGlyLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
DB 227 GTGAGAGAAAAACAAGTCCATTTTTTTGTAATGTCATCTGATGTCGACCAATGTGAAGCC 286
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Qy 61 HisLeuAenValSerGlylleProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
 Db 287 CATTTAAATGTGAGCGGAATTCATGTCAGTCTTGTGGCAGACGTGGAAGATCTTTATT 346  
 Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
 Db 347 CAACAGCAGATTTCCACGACACAGTCAGCCCCCGAGCTCCGATCGTACTATGACAG 406  
 Qy 101 TyrHisSerLeuAenGluileTyrSerTrpIleGluPheileThrGluArgHisProAsp 120  
 Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTATAACTGAGAGCATCTCTGAT 466  
 Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
 Db 467 ATGCTTACAAAAATCCACATTTGGATTCCTATTGAGAAGTAGTACCACCTCTATGTTTAAAG 526

RESULT 8

US-10-115-479-69  
 ; Sequence 69, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glendda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Malyanker, Uriel W.  
 ; APPLICANT: Shinkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-322 B (Cura 622 FT)  
 ; CURRENT APPLICATION NUMBER: US/10/115,479  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,687  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; PRIOR APPLICATION NUMBER: 60/285,325  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 198  
 ; SEQ ID NO 69  
 ; LENGTH: 1344  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (31)..(1315)  
 ; US-10-115-479-69  
 Alignment Scores:  
 Pred. No.: 5,79e-136 Length: 1344  
 Score: 140.00 Matches: 140  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 41.42% Indels: 0  
 DB: 16 Gaps: 0  
 US-09-980-881A-3 (1-338) x US-10-115-479-69 (1-1344)  
 Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
 Db 97 TTTTCAGAGTGGCCAAAGTTCTAGCTGTCTTCTTAGAACTCTTAGGCAAGTTCAAGTTCTA 156  
 Qy 21 GlnAsnLeuThrThrTyrGluileValLeuTrpGlnProValThrAlaAspLeuile 40  
 Db 157 CAGAATCTTACTACACATATGAGATTGTCTCTGGCAGCGGTAACAGCTGACCTTATT 216  
 Qy 41 VallyslylsGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60  
 Db 217 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAAGCC 276  
 Qy 61 HisLeuAenValSerGlylleProCysSerValLeuLeuAlaAspValGluAspLeuile 80  
 Db 277 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGTGGCAGACGTGGAAGATCTTTATT 336  
 Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
 Db 337 CAACAGCAGATTTCCACGACACACAGTCAGCCCCCGAGCTCCGATCGTACTATGACAG 396  
 Qy 101 TyrHisSerLeuAenGluileTyrSerTrpIleGluPheileThrGluArgHisProAsp 120  
 Db 397 TATCACTCACTAAATGAATCTATTCTTGGATAGATTTATAACTGAGAGCATCTCTGAT 456  
 Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
 Db 457 ATGCTTACAAAAATCCACATTTGGATTCCTATTGAGAAGTAGTACCACCTCTATGTTTAAAG 516

RESULT 9

US-10-115-479-67  
 ; Sequence 67, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glendda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna

```
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:
Pred. No.: 7,398-136 Length: 1743
Score: 140.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.42% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-115-479-67 (1-1743)

QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
DB 86 TTTCAGAGTGGCCAGTTCTAGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 145
QY 21 GlnAsnLeuThrThrThrGluLeuValLeuThrGlnProValThrAlaAspLeuLeu 40
DB 146 CAGAACTTACTACAACATATGAGATTGTCTCTGGCAGCCGGTAACAGCTGACCTTAT 205
QY 41 VallyslslyslsGlnValHisPheValAsnAspValAspValValysAla 60
DB 206 GTGAAGAAAAAACAAGTCCATTTTGTAAATGTCATCTGTGTCACAAATGGAAGCC 265
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80
DB 266 CATTTAAATGTAGCGGAATTCATGCTGTCTGTCGACAGCTGGGAAGATCTTATT 325
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
DB 326 CAACAGCAGATTTCACACGACACAGTCAGCCCCCAGCCTCCGATCTGTAATGACAG 385
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
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DB 386 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTATAACTGAGGCGATCCTGAT 445
QY 121 MetLeuThrIysIleHisIleGlySerSerPheGluIysTyrProLeuTyrValLeuIys 140
DB 446 ATGCTTACAAAAATCCACATTTGGAATTCCTCAITTTGAGAAAGTACCCACTCTATGTTTAAAG 505

RESULT 10
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Alignment Scores:
Pred. No.: 2,838-59 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.12% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-3 (1-338) x US-09-813-133A-3 (1-55827)

QY 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226
DB 48643 GAGGAAGTGTCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCA 48702
QY 227 GluProGluValIysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleIysAla 246
DB 48703 GAACCAAGAGTGAGGCGAGTGGCTAGTTCTTTGAGAAGAAATATCAACAGATTAAGCA 48762
QY 247 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 266
DB 48763 TACATCAGATGATTCATCATCTCCAGCATATAGTGTTCATATTCCTATATACACGAGT 48822
QY 267 LysSerLysAspHisGluGluLeu 274
DB 48823 AAAAGCAAGACCATGAGGAAGCTG 48846

RESULT 11
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinlu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
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## US-10-212-877-3

## Alignment Scores:

Pred. No.: 2,83e-59 Length: 55827  
Score: 68.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.12% Indels: 0  
DB: 14 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-212-877-3 (1-55827)

Qy 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226  
Db 48643 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 48702  
Qy 227 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246  
Db 48703 GAACCAAGTGAAGGCACTGGTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 48762  
Qy 247 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 266  
Db 48763 TACATCAGATGCATTCATCTACTCCAGCATATAGTGTTCATATTCATATACACGAAGT 48822  
Qy 267 LysSerLysAspHisGluGluLeu 274  
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

## RESULT 12

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

## Alignment Scores:

Pred. No.: 1.81e-52 Length: 1272  
Score: 60.00 Matches: 60  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 17.75% Indels: 0  
DB: 15 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-379-836-1 (1-1272)

Qy 53 SerAspValAspAsnValLysAlaHisLeuAsnValSerGlyIleProCysSerValLeu 72  
Db 223 TCTGATGTCGCAATGTGAAGCCCATTTAAATGTGAGCGGAATTCATGCGAGTCTCTG 282  
Qy 73 LeuAlaAspValGluAspLeuIleGlnGlnIleSerAsnAspThrValSerProArg 92  
Db 283 CTGGCAGATGTGAAGATCTTATTCAACAGCAGATTTCCAAACAGACACAGTCAGCCCCCGA 342  
Qy 93 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 112  
Db 343 GCCTCCGATCGTACTATGAACAGATATCACTCACTAAATGAATCTATTCTTGGATAGAA 402

## RESULT 13

US-10-027-632-265133  
; Sequence 265133, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 265133  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1547)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-265133

## Alignment Scores:

Pred. No.: 1.21e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.72% Indels: 0  
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265133 (1-1547)

Qy 207 GluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSer 226  
Db 1417 GAGGAAGTGCATCCAGTCTCTCATGCTCGGAACCTACTGTGGACTTTATCCTGAGTCA 1476  
Qy 227 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246  
Db 1477 GAACCAAGTGAAGGCACTGGTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536  
Qy 247 TyrIleSer 249  
Db 1537 TACATCAGC 1545

## RESULT 14

US-10-027-632-265134  
; Sequence 265134, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12



;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 265134  
;; TYPE: DNA  
;; ORGANISM: Human  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (1)...(1547)  
;; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-265134

Alignment Scores:  
Pred. No.: 1,21e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.72% Indels: 0  
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265134 (1-1547)

QY 207 GluGluGlyAlaSerSerSerSerSerGluThrTyxCysGlyLeuTyProGluSer 226  
|||  
Db 1417 GAGGAAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTATCTGAGTCA 1476  
  
QY 227 GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246  
|||  
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536  
  
QY 247 TyrIleSer 249  
|||  
Db 1537 TACATCAGC 1545

RESULT 15  
US-10-027-632-265135  
;; Sequence 265135, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; TITLE OF INVENTION: Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 265135  
;; LENGTH: 1547  
;; TYPE: DNA  
;; ORGANISM: Human  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (1)...(1547)  
;; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-265135  
  
Alignment Scores:  
Pred. No.: 1,21e-34 Length: 1547  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.72% Indels: 0  
DB: 13 Gaps: 0

US-09-980-881A-3 (1-338) x US-10-027-632-265135 (1-1547)  
  
QY 207 GluGluGlyAlaSerSerSerSerSerGluThrTyxCysGlyLeuTyProGluSer 226  
|||  
Db 1417 GAGGAAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTATCTGAGTCA 1476  
  
QY 227 GluProGluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 246  
|||  
Db 1477 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 1536  
  
QY 247 TyrIleSer 249  
|||  
Db 1537 TACATCAGC 1545

Search completed: October 27, 2004, 09:21:14  
Job time : 501.441 secs



Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	57	3.2	19	3	US-09-309-317-5	Sequence 5, Appli
2	42.5	2.4	16	4	US-09-541-345-44	Sequence 44, Appl
3	40	2.2	18	4	US-09-693-822B-19	Sequence 19, Appl
4	40	2.2	19	4	US-09-693-822B-8	Sequence 8, Appli
5	40	2.2	19	4	US-09-693-822B-23	Sequence 23, Appl
6	40	2.2	19	4	US-09-693-822B-24	Sequence 24, Appl
7	39.5	2.2	13	4	US-09-402-641-1	Sequence 1, Appli
8	39.5	2.2	15	3	US-08-142-590B-5	Sequence 5, Appli
9	39.5	2.2	18	2	US-08-747-915-4	Sequence 4, Appli
10	39.5	2.2	18	3	US-08-467-023-211	Sequence 211, App
11	39.5	2.2	18	3	US-08-142-590B-4	Sequence 4, Appli
12	39.5	2.2	18	3	US-08-142-590B-24	Sequence 24, Appl
13	39.5	2.2	18	4	US-09-285-783-4	Sequence 4, Appli
14	39	2.2	13	2	US-08-596-387B-6	Sequence 6, Appli
15	39	2.2	13	3	US-09-067-615-6	Sequence 6, Appli
16	39	2.2	13	5	PCT-US95-09816A-6	Sequence 6, Appli
17	39	2.2	17	1	US-08-428-733A-55	Sequence 55, Appl
18	39	2.2	18	4	US-08-634-332A-2	Sequence 2, Appli
19	39	2.2	19	4	US-09-693-822B-25	Sequence 25, Appl
20	38.5	2.1	17	4	US-09-622-624-20	Sequence 20, Appl
21	38	2.1	14	2	US-08-685-589A-198	Sequence 198, App
22	38	2.1	16	4	US-09-340-620A-47	Sequence 47, Appl
23	38	2.1	17	2	US-08-685-589A-140	Sequence 140, App
24	38	2.1	17	4	US-08-482-967-25	Sequence 25, Appl
25	38	2.1	18	5	PCT-US93-0374B-10	Sequence 10, Appl
26	38	2.1	19	1	US-08-382-013A-59	Sequence 59, Appl
27	38	2.1	19	1	US-08-382-013A-71	Sequence 71, Appl

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CEA binding
; OTHER INFORMATION: polypeptide
US-09-541-345-44

Query Match          2.4%; Score 42.5; DB 4; Length 16;
Best Local Similarity 43.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 152 IWIDCGIHAREWISPA 167
    ||| : : : |||
Db 1 IW-DCNLFKNQWFCPA 15

RESULT 3
US-09-693-822B-19
; Sequence 19, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-19

Query Match          2.2%; Score 40; DB 4; Length 18;
Best Local Similarity 38.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
    :||| : : : |||
Db 2 HHC-----YKRKFPEKHCHRG 18

RESULT 4
US-09-693-822B-8
; Sequence 8, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-8

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
    :||| : : : |||

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Db 2 HHC-----YKRKFPEKHCHRG 18

RESULT 5
US-09-693-822B-23
; Sequence 23, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-23

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
    :||| : : : |||
Db 2 HHC-----YKRKFPEKHCHRG 18

RESULT 6
US-09-693-822B-24
; Sequence 24, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-24

Query Match          2.2%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 1; Mismatches 8; Indels 4; Gaps 1;

Qy 189 NHCIGTDLNRNFASKHWCEEG 209
    :||| : : : |||
Db 2 HHC-----YKRKFPEKHCHRG 18

RESULT 7
US-09-402-641-1
; Sequence 1, Application US/09402641
; Patent No. 6528619
; GENERAL INFORMATION:
; APPLICANT: BUERGLE, Markus
; APPLICANT: GRAEPF, Heinrich

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; APPLICANT: KESSLER, Horst
; APPLICANT: MAGDOLEN, Viktor Robert
; APPLICANT: KOENIG, Bernhard
; APPLICANT: KOPFITZ, Marcus
; APPLICANT: RIEMER, Christoph
; APPLICANT: SCHMITT, Manfred
; APPLICANT: WEIDLE, Ulrich
; APPLICANT: WILHELM, Olaf
; TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR
; FILE REFERENCE: Case 20367US
; CURRENT APPLICATION NUMBER: US/09/402,641
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: EP97106024.9
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/EP98/02178
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide "cyclo
; OTHER INFORMATION: 19.31 UPA 19-31", Figure 3A
US-09-402-641-1

Query Match      2.2%; Score 39.5; DB 4; Length 13;
Best Local Similarity 37.5%; Pred. No. 7.8e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 1 CVS---NKYFSNIHWC 13

RESULT 8
US-08-142-590B-5
; Sequence 5, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and GOETINCK,
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-142-590B-5

Query Match      2.2%; Score 39.5; DB 3; Length 15;
Best Local Similarity 37.5%; Pred. No. 9.8e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 2 CVS---NKYFSNIHWC 14

RESULT 9
US-08-747-915-4
; Sequence 4, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEFAX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-747-915-4

Query Match      2.2%; Score 39.5; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 191 CIGTDLNRNPFASKHWC 206
Db 3 CVS---NKYFSNIHWC 15

RESULT 10
US-08-467-023-211
; Sequence 211, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;

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Query Match 2.2%; Score 39.5; DB 3; Length 18;  
Best Local Similarity 37.5%; Pred. NO. 1.3e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNRNFASKHWC 206  
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Db 4 CVS---NKYFSNIHWC 16

RESULT 13  
US-09-285-783-4  
; Sequence 4, Application US/09285783  
; Patent No. 6514710  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; Haney, David N.  
; Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RADER, FISHMAN & GRAUER  
; STREET: 1233 20TH STREET NW, SUITE 501  
; CITY: WASHINGTON

Query Match 2.2%; Score 39.5; DB 4; Length 18;  
Best Local Similarity 37.5%; Pred. NO. 1.3e+03;  
Matches 6: Conservative 4; Mismatches 3; Indels 3; Gaps 1;

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Qy      191 CIGTDLNRNFASKHWC 206
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Db      3 CVS---NKYFSNIHWC 15

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RESULT 14
US-08-596-387B-6
; Sequence 6, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiao, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124

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CORRESPONDENCE ADDRESS:  
ADDRESS: Bade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596.387B  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/09816  
FILING DATE: 31-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-08-596-387B-6

Query Match 2.2%; Score 39; DB 2; Length 13;  
Best Local Similarity 58.3%; Pred. No. 8.9e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels

Qy 63 NVSGIPCSVLLA 74  
|: |||||  
Db 1 NLCNIPCSALLS 12

RESULT 15  
US-09-067-615-6  
; Sequence 6, Application US/09067615  
; Patent No. 6309645  
; GENERAL INFORMATION:  
; APPLICANT: Rhode, Peter R.  
; APPLICANT: Jiao, Jin-An  
; APPLICANT: Burkhardt, Martin  
; APPLICANT: Wong, Hing  
; TITLE OF INVENTION: MHC COMPLEXES AND USSES THEREOF  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/067.615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596.387
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382.454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283.302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-09-067-615-6

Query Match      2.2%; Score 39; DB 3; Length 13;
Best Local Similarity 58.3%; Pred. NO. 8.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      63 NVSGIPCSVLIA 74
Db      1 NLCNIPCSALLS 12

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Search completed: October 27, 2004, 01:31:43  
Job time : 18.5445 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:13:21 ; Search time 42.6081 Seconds  
(without alignments)  
2568.304 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 1798  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYFSTNPPEVKLPLSLK 338

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 260209

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	57	3.2	19	9 US-09-799-760-5	Sequence 5, Appli
2	48	2.7	11	16 US-10-343-509-10	Sequence 10, Appl
3	46	2.6	11	15 US-10-410-764-87	Sequence 87, Appl
4	42.5	2.4	16	10 US-09-825-517A-44	Sequence 44, Appl
5	41	2.3	13	15 US-10-469-304-55	Sequence 55, Appl
6	41	2.3	18	16 US-10-742-379-90	Sequence 90, Appl
7	40	2.2	14	15 US-10-436-715-431	Sequence 431, Appl
8	39.5	2.2	13	16 US-10-756-289-3	Sequence 3, Appli
9	39.5	2.2	15	16 US-10-756-289-2	Sequence 2, Appli
10	39.5	2.2	18	14 US-10-349-543-4	Sequence 4, Appli
11	39.5	2.2	19	10 US-09-791-524-1	Sequence 1, Appli
12	39	2.2	13	9 US-09-848-164-6	Sequence 6, Appli
13	39	2.2	13	9 US-09-957-674-5	Sequence 5, Appli

14	39	2.2	13	9 US-09-900-379-6	Sequence 6, Appli
15	39	2.2	19	10 US-09-791-524-2	Sequence 20, Appli
16	38.5	2.1	17	9 US-09-822-624-20	Sequence 2, Appl
17	38	2.1	16	9 US-09-728-721-47	Sequence 47, Appl
18	38	2.1	16	14 US-10-295-981-47	Sequence 47, Appl
19	38	2.1	18	14 US-10-125-869A-23	Sequence 23, Appl
20	38	2.1	18	15 US-10-462-262-247	Sequence 247, App
21	38	2.1	18	16 US-10-364-645A-54	Sequence 54, Appl
22	38	2.1	19	8 US-08-817-832B-25	Sequence 25, Appl
23	38	2.1	19	15 US-10-440-435-25	Sequence 25, Appl
24	37.5	2.1	15	14 US-10-034-974-32	Sequence 32, Appl
25	37.5	2.1	17	15 US-10-624-153-66	Sequence 66, Appl
26	37.5	2.1	18	16 US-10-712-447-22	Sequence 22, Appl
27	37	2.1	13	15 US-10-469-304-56	Sequence 56, Appl
28	37	2.1	14	9 US-09-740-211-15	Sequence 15, Appl
29	37	2.1	14	13 US-10-007-968-15	Sequence 15, Appl
30	37	2.1	14	14 US-10-293-400-15	Sequence 15, Appl
31	37	2.1	15	14 US-10-371-540-30	Sequence 30, Appl
32	37	2.1	15	16 US-10-327-598-74	Sequence 74, Appl
33	37	2.1	16	14 US-10-225-567A-1864	Sequence 1864, Ap
34	37	2.1	16	14 US-10-083-768-15	Sequence 15, Appl
35	37	2.1	16	15 US-10-609-217-75	Sequence 75, Appl
36	37	2.1	16	15 US-10-632-388-75	Sequence 75, Appl
37	37	2.1	16	15 US-10-651-723-75	Sequence 75, Appl
38	37	2.1	16	15 US-10-645-761-75	Sequence 75, Appl
39	37	2.1	16	15 US-10-666-696-75	Sequence 75, Appl
40	37	2.1	16	15 US-10-653-048-75	Sequence 75, Appl
41	37	2.1	18	14 US-10-105-232-194	Sequence 194, App
42	37	2.1	18	14 US-10-189-437-181	Sequence 181, App
43	37	2.1	19	9 US-09-864-761-41546	Sequence 41546, A
44	37	2.1	19	10 US-09-931-325A-25	Sequence 25, Appl
45	37	2.1	19	10 US-09-563-222-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1  
US-09-799-760-5  
; Sequence 5, Application US/09799760  
; Patent No. US20010021771A1  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley  
; APPLICANT: Tremblay, Patrick  
; APPLICANT: Moore, Richard  
; APPLICANT: Westaway, David  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Lee, Inyoul  
; TITLE OF INVENTION: PrP-like Gene  
; FILE REFERENCE: 6510-130CON  
; CURRENT APPLICATION NUMBER: US/09/799,760  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 09/309,317  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized peptide  
US-09-799-760-5

Query Match 3.2%; Score 57; DB 9; Length 19;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 189 NHCIGTDLNRNFASKHWC 206  
Db 1 NHCFGAEGNRYAANYIC 18

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RESULT 2
US-10-343-509-10
; Sequence 10, Application US/10343509
; Publication No. US20040101865A1
; GENERAL INFORMATION:
; APPLICANT: BASF
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
; FILE REFERENCE: 0050/51654
; CURRENT APPLICATION NUMBER: US/10/343,509
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Euglena gracilis
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = (Phe/Tyr)
US-10-343-509-10

Query Match          2.7%; Score 48; DB 16; Length 11;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 309 GGDWYDLG 318
Db 1 GGDGWYDIG 10

RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match          2.6%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 251 HSYSQHIVFPY 261
Db 1 HSYSQMLMPY 11

RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421, 1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match          2.4%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred. No. 3.1e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 152 IWIDGIIHAREWISPA 167
Db 1 IW-DCNLFKQWFCPA 15

RESULT 5
US-10-469-304-55
; Sequence 55, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
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US-10-469-304-55

Query Match 2.3%; Score 41; DB 15; Length 13;  
Best Local Similarity 42.1%; Pred. No. 3.2e+03;  
Matches 8; Conservative 2; Mismatches 1; Indels 8; Gaps 1;

Qy 31 LWQPVTDLIVKKKQVHFF 49  
Db 2 LWQPVTDLIVKKKQVHFF 12

RESULT 6

US-10-742-379-90  
; Sequence 90, Application US/10742379  
; Publication No. US20040181033A1  
; GENERAL INFORMATION:  
; APPLICANT: Han, HQ  
; APPLICANT: Min, Hoshung  
; APPLICANT: Boone, Thomas Charles  
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN  
; FILE REFERENCE: A-828 (US)  
; CURRENT APPLICATION NUMBER: US/10/742,379  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/435,923  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 634  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 90  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Myostatin Binding Peptide  
US-10-742-379-90

Query Match 2.3%; Score 41; DB 16; Length 18;  
Best Local Similarity 83.3%; Pred. No. 5.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 204 HMCCEG 209  
Db 2 HMCCEG 7

RESULT 7

US-10-436-715-431  
; Sequence 431, Application US/10436715  
; Publication No. US20040018976A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
; TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF  
; FILE REFERENCE: D0262 NP  
; CURRENT APPLICATION NUMBER: US/10/436,715  
; PRIOR FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: U.S. 60/380,336  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 471  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-436-715-431

Query Match 2.2%; Score 40; DB 15; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.5e+03;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 NLATTVEIVLWQ 33  
Db 3 DLNTGYDVVLWK 14

RESULT 8

US-10-756-289-3  
; Sequence 3, Application US/10756289  
; Publication No. US20040138110A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitt, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/10/756,289  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US/09/402,464  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 1...12  
; OTHER INFORMATION: D-amino acids may be substituted for corresponding L-  
; OTHER INFORMATION: amino acids at  
; OTHER INFORMATION: positions 1,2,3,9, 11, and 12.  
US-10-756-289-3

Query Match 2.2%; Score 39.5; DB 16; Length 13;  
Best Local Similarity 37.5%; Pred. No. 4.6e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNRFASKWC 206  
Db 1 CVSS---NKYFSNIHWC 13

RESULT 9

US-10-756-289-2  
; Sequence 2, Application US/10756289  
; Publication No. US20040138110A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitt, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/10/756,289  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US/09/402,464  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-756-289-2

Query Match 2.2%; Score 39.5; DB 16; Length 15;

Best Local Similarity 37.5%; Pred. No. 5.6e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNRNFASKHWC 206  
|: |: |: ||  
Db 2 CVS---NKYFSNIHWC 14

RESULT 10

US-10-349-543-4  
; Sequence 4, Application US/10349543  
; Publication No. US20030166514A1  
; GENERAL INFORMATION:

Query Match 2.2%; Score 39.5; DB 14; Length 18;  
Best Local Similarity 37.5%; Pred. No. 7.3e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 191 CIGTDLNRNFASKHWC 206  
| : | : | : |  
Db 3 CVS--NKYFSNIHWC 15

RESULT 11

US-09-791-524-1  
; Sequence 1, Application US/09791524  
; Publication No. US20030143209A1  
; GENERAL INFORMATION:

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; PRIOR APPLICATION NUMBER: 60/098288
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: prt
; ORGANISM: Adenovirus
; US-09-791-524-1

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Qy 191 CIGTDLNRNFASKHWC 206  
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Db 6 CVS---NKYFSNIHWC 18

RESULT 12

US-09-848-164-6  
; Sequence 6, Application US/09848164  
; Patent No. US20020034513A1

Query Match 2.2%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels

QY 63 NVSGIPCSVILLA 74  
|: ||||| |:  
Db 1 NLCNIPCSALLS 12

RESULT 13  
US-09-957-674-5  
; Sequence 5, Application US/09957674  
; Patent No. US20020120948A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Methods for Expressing Gene Products  
; FILE REFERENCE: 18396/2072  
; CURRENT APPLICATION NUMBER: US/09/957,674  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB990736  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/01225  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 5  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Chicken  
US-09-957-674-5

Query Match 2.2%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 63 NVSGIPCSVILLA 74  
|: ||||| |:  
Db 1 NLCNIPCSALLS 12

RESULT 14  
US-09-900-379-6  
; Sequence 6, Application US/09900379  
; Publication No. US20020198144A1  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; Rhode, Peter R.  
; Widanz, Jon A.  
; Grammer, Susan  
; Edwards, Ana C.  
; Chavallaz, Pierre-Andre  
; Jiao, Jin-An  
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
; NUMBER OF SEQUENCES: 123  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dade International, Inc.  
; STREET: 1717 Deerfield Road  
; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/900,379  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,084  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/US95/09816  
; FILING DATE: 31-JUL-1995  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995

APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 2.2%; Score 39; DB 9; Length 13;  
Best Local Similarity 58.3%; Pred. No. 5.1e+03;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 63 NVSGIPCSVILLA 74  
|: ||||| |:  
Db 1 NLCNIPCSALLS 12

RESULT 15  
US-09-791-524-2  
; Sequence 2, Application US/09791524  
; Publication No. US20030143209A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharmaceuticals Products Inc.  
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
; FILE REFERENCE: A3319A  
; CURRENT APPLICATION NUMBER: US/09/791,524  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/09828  
; PRIOR FILING DATE: 1998-08-27  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Adenovirus  
US-09-791-524-2

Query Match 2.2%; Score 39; DB 10; Length 19;  
Best Local Similarity 50.0%; Pred. No. 8.9e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 197 NRNFASKHWC 206  
|: ||: ||| |:  
Db 9 NKYFSNIHWC 18

Search completed: October 27, 2004, 01:43:16  
Job time : 42.6081 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 27, 2004, 01:43:22 ; Search time 88.7966 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

Title: US-09-980-881A-3  
Perfect score: 1798  
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYSFTSNPPVKKLPLSLK 338

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents\_NA.\*  
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5: /cgn2\_6/prodata/1/ina/6C COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/6D COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749.5	97.3	1625	US-09-813-133A-1	Sequence 1, Appli
2	1732	96.3	1272	US-08-869-057-1	Sequence 1, Appli
3	1732	96.3	1749	US-07-649-591B-2	Sequence 2, Appli
4	1732	96.3	1749	US-08-277-540-2	Sequence 2, Appli
5	1732	96.3	1749	US-08-430-787A-2	Sequence 2, Appli
6	646.5	36.0	1215	US-08-696-139-1	Sequence 1, Appli
7	637.5	35.5	1263	US-08-860-882A-56	Sequence 56, Appli
8	637.5	35.5	1263	US-09-011-769A-38	Sequence 38, Appli
9	637.5	35.5	1284	US-08-860-882A-71	Sequence 71, Appli
10	637.5	35.5	1284	US-09-011-769A-55	Sequence 55, Appli
11	622	34.6	1622	US-09-023-655-1020	Sequence 1020, Ap
12	619.5	34.5	1311	US-09-675-305-9	Sequence 9, Appli

13	619.5	34.5	1311	4	US-10-200-344-9	Sequence 9, Appli
14	619.5	34.5	2154	3	US-09-171-945-124	Sequence 124, App
15	610	33.9	927	2	US-08-782-760-5	Sequence 5, Appli
16	610	33.9	927	5	PCT-US96-00995-5	Sequence 5, Appli
17	582	22.4	921	1	US-08-696-139-3	Sequence 3, Appli
18	571.5	31.8	921	4	US-09-675-305-13	Sequence 13, Appl
19	571.5	31.8	2128	4	US-10-200-344-13	Sequence 13, Appl
20	567	31.5	999	2	US-08-860-882A-67	Sequence 67, Appl
21	567	31.5	999	4	US-09-011-769A-50	Sequence 50, Appl
22	567	31.5	1053	2	US-08-860-882A-64	Sequence 64, Appl
23	567	31.5	1053	4	US-09-011-769A-46	Sequence 46, Appl
24	560	31.1	1053	4	US-09-463-451-27	Sequence 27, Appl
25	560	31.1	1053	4	US-09-463-451-28	Sequence 28, Appl
26	560	31.1	1059	2	US-08-860-882A-74	Sequence 74, Appl
27	560	31.1	1059	4	US-09-011-769A-59	Sequence 59, Appl
28	559	31.1	1059	2	US-08-860-882A-77	Sequence 77, Appl
29	559	31.1	1059	4	US-09-011-769A-63	Sequence 63, Appl
30	554	30.8	1200	4	US-09-710-099-7	Sequence 7, Appli
31	554	30.8	1200	4	US-10-200-910-7	Sequence 7, Appli
32	549	30.5	1870	3	US-09-171-945-112	Sequence 112, App
33	534.5	29.7	1050	4	US-09-675-305-11	Sequence 11, Appl
34	534.5	29.7	1050	4	US-10-200-344-11	Sequence 11, Appl
35	527.5	29.3	1311	4	US-09-710-099-5	Sequence 5, Appli
36	527.5	29.3	1311	4	US-10-200-910-5	Sequence 5, Appli
37	516.5	28.7	1251	3	US-08-640-906-3	Sequence 3, Appli
38	516.5	28.7	1251	3	US-09-395-936-3	Sequence 3, Appli
39	491.5	27.3	1257	3	US-08-640-906-1	Sequence 1, Appli
40	491.5	27.3	1257	3	US-09-395-936-1	Sequence 1, Appli
41	467.5	26.0	945	4	US-09-710-099-3	Sequence 3, Appli
42	467.5	26.0	945	4	US-09-710-099-11	Sequence 11, Appl
43	467.5	26.0	945	4	US-10-200-910-3	Sequence 3, Appli
44	467.5	26.0	945	4	US-10-200-910-11	Sequence 11, Appl
45	465.5	25.9	2247	4	US-09-710-099-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

Alignment Scores:  
Pred. No.: 3,19e-215 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservative: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 4 Gaps: 1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

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Db	83	TTTCAGATGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA	142
QY	21	GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle	40

Db 143 CAGAACTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 202  
Qy 41 VallylsylsGlnValHisPheValAsnAlaSerAspValAspAsnVallyAla 60  
Db 203 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 262  
Qy 61 HisLeuAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTGTGGCAGATGTGGAAGATCTTATT 322  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTCCACAGCACACAGTCAGCCCCCGAGCCTCCGATCGTACTATGAACAG 382  
Qy 101 TyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACATAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGCATCTTGAT 442  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTACAAAAATCCACATTTGATCTCTCATTTGAGAAGTACCCACTCTATGTTTTAAAG 502  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTCTGGAAAAAGAACAGACGACCAAAATGCCATATGGATTGACTGTGGAAATCCATGCC 562  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMeTrpArg 180  
Db 563 AGAGAAATGGATCTCTCTGCTTCTGCTTGTGGTTTCATAGGCCATAATCGAATGTGGAGA 622  
Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGTCTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAAATAGGAACCTTT 682  
Qy 201 AlaSerLysHisTrpCysGluGluAlaSerSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGGTGTGAGNAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGT 742  
Qy 221 GlyLeuTyrProGluSerGluProGluVallyAlaValAlaSerPheLeuArgArgAsn 240  
Db 743 GGACTTTATCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCCTTCTGAGAAGAAAT 802  
Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACAGATTAAGACATACATCAGCATGATTCATCTACTCCAGCATATAGTGTTCGA 862  
Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCCTATACAGAAATTAAGCAAGAACCATGAGGAACGTCTCTAGTAGCCAGTGAA 922  
Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCGTGCTATTGAGAAAAATAGTAAAAATACCAGGTATACACATGGCCATGGCTCA 982  
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyLeuLys 320  
Db 983 GAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTCGATATGATTTGGGCATCAA 1042  
Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCGTTTACAATTGAATTCGAGATCGGGACACATACGGAATCTTCTGCTCCCGAGCGT 1102  
Qy 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCTAAAA 1148

## RESULT 2

US-08-869-057-1  
; Sequence 1, Application US/08869057  
; Patent No. 5985562  
; GENERAL INFORMATION:  
; APPLICANT: Morser, Michael J  
; APPLICANT: Nagashima, Mariko

; TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
; TITLE OF INVENTION: Risk  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berlex Biosciences Legal Department  
; STREET: 15049 San Pablo Avenue  
; CITY: Richmond  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94804-0099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; APPLICATION NUMBER: US/08/869,057  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Washtien, Wendy L  
; REGISTRATION NUMBER: 36,301  
; REFERENCE/DOCKET NUMBER: 51509AUSM1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-5411  
; TELEFAX: 510-262-7095  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1272 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PUBLICATION INFORMATION:  
; AUTHORS: Eaton, Dan L.  
; AUTHORS: Malloy, Beth E.  
; AUTHORS: Tsai, Siao P  
; AUTHORS: Henzel, William  
; AUTHORS: Drayna, Dennis  
; TITLE: Isolation, Molecular Cloning, and Partial  
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B  
; TITLE: from Human Plasma  
; JOURNAL: J. Biol. Chem.  
; VOLUME: 266  
; ISSUE: 32  
; PAGES: 21833-21838  
; DATE: No. 5985562 15-1991  
; US-08-869-057-1  
  
Alignment Scores:  
Pred. No.: 3.8e-213 Length: 1272  
Score: 1732.00 Matches: 338  
Percent Similarity: 86.01% Conservative: 0  
Best Local Similarity: 86.01% Mismatches: 0  
Query Match: 96.33% Indels: 55  
DB: 2 Gaps: 2  
  
US-09-980-881A-3 (1-338) x US-08-869-057-1 (1-1272)  
  
Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnVal 20  
Db 67 TTTCCAGAGTGGCCAAAGTTCTAGCTGCTCTCTTAGAACCTCTAGCAAGTTCAAGTTCTA 126  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 40  
Db 127 CAGAATCTTACTACACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 186  
Qy 41 VallylsylsGlnValHisPheValAsnAlaSerAspValAspAsnVallyAla 60  
Db 187 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAGCC 246  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80



Db 247 CATTAAATGTGAGCGGAATTCATGCAGTGTCTTGCTGGCAGACGCTGGAAGATCTTATT 306  
 Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
 Db 307 CAACAGCAGATTTCCACGACACACAGTACGCCCGGAGCTCCGCATCGCTATATGAACAG 366  
 Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
 Db 367 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTAATCACTGAGAGCATCTTGAT 426  
 Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
 Db 427 ATGCTTACAAAAATCCACATGGATCTCTCATTTGAGAAAGTACCCCACTCTATGTTTTAAAG 486  
 Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIleHisAla 160  
 Db 487 GTTCTGGAAGAAGAACCAACGCAAAATGCCATATGGATTGACTGGGAATCCATGCC 546  
 Qy 161 ArgGluTyrIleSerProAlaPheCysLeuTyrPheIleGlyHis----- 175  
 Db 547 AGAAGATGGATCTCTCTGCTTCTGCTTGGTTTCATAGGCCATATACTCAATTTCTAT 606  
 Qy 175 ----- 175  
 Db 607 GCGATAATAGGCAATATACCAATCTCCTGAGGCTTGTGGATTTCTATGTTATGCCGCTG 666  
 Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
 Db 667 GTTAATGTGACGGTTATGACTACTCATGGAAGAAATCGAATGTGGAGAAAGAACCGT 726  
 Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
 Db 727 TCTTTCTATGCCAACAATCATTTGCATCGAACAGACCTGAATAGGAACCTTGTCTCCAAA 786  
 Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
 Db 787 CACTGGTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTAT 846  
 Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243  
 Db 847 CCGTAGTCAGAACCAAGAGTGAAGCGAGTGGCTAGTTCTTGAGAGAAATATCAACCCAG 906  
 Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
 Db 907 ATTAAGCATATCATCAGCATGATTCATCTACTCCAGCATATAGTGTTCATATTCCTAT 966  
 Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
 Db 967 ACACGAAGTAAAGCAAGCAACCATGAGGAACGTCTCTAGTAGCCAGTGAAGCAGTTCT 1026  
 Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
 Db 1027 GCTATTGAGAAAACTAGTAAAAATACCAAGGTATACATGCGCATGGCTCAGAAACCTTA 1086  
 Qy 304 TyrLeuAlaProGlyGlyLysAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
 Db 1087 TACCTAGTCTCTGGAGGTGGGACGATTTGAUCTATGATTTGGGCATCAAAATATTCGTT 1146  
 Qy 324 -----ThrSerAs 326  
 Db 1147 ACAATTTGAATTCGAGATAGGGCACATACCGGATTTCTTGCTGGCGAGGCTTACATCAAA 1206  
 Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338  
 Db 1207 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1243

RESULT 3

US-07-649-591B-2  
 ; Sequence 2, Application US/07649591B  
 ; Patent No. 5206161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis Drayna and Daniel Eaton  
 ; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase

NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/649,591B  
 FILING DATE: 19910201  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/266-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1749 bases  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: hybridization probe  
 LOCATION: 133 to 178  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 FEATURE:  
 NAME/KEY: potential clip site  
 LOCATION: 380 to 382  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: 41 to 106  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:

Alignment Scores:  
 Pred. No.: 6,588-213 Length: 1749  
 Score: 1732.00 Matches: 338  
 Percent Similarity: 86.01% Conservative: 0  
 Best Local Similarity: 86.01% Mismatches: 0  
 Query Match: 96.33% Indels: 55  
 DB: 1 Gaps: 2

US-09-980-881A-3 (1-338) x US-07-649-591B-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
 Db 107 TTTTCAGAGTGGCCAAAGTTCTAGCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166  
 Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 40  
 Db 167 CAGAACTCTTACTACAAACATATGAGATTGTCTCTGGCAGCCGGTAAACAGCTGACCTTATT 226  
 Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
 Db 227 GTGAAGAAAAAACAAGTCCATTTTTTTTGTAAATGTCATCTGTGTCACATATGTGAAGCC 286

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Qy 61 HisLeuAenValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80
Db 287 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTTGCGCAGAGCTGGAAGATCTTATT 346

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTCCAAACGACACACAGTACGCCCGAGCTCCGATCGTACTATGAACAG 406

Qy 101 TyrHisSerLeuAenGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTATAACTGAGAGCATCTTGAT 466

Qy 121 MetLeuThrIleHisIleGlySerSerPheGluIleTyrProLeuTyrValLeuIlys 140
Db 467 ATGCTTACAAAATCCACATTGGATCCCTATTGAGAAAGTACCCCACTCTATGTTTTAAAG 526

Qy 141 ValSerGlyIysGluGlnThrAlaIysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTCTGGAAGAACAACAGCCAAATGCCATATGGATTGACTGTGGAAATCCATGCC 586

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAGAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAAATCAATCTTAT 646

Qy 175 ----- 175

Db 647 GGGTAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706

Qy 176 -----AsnArgMetTrpArgIysAsnArg 183
Db 707 GTTAATGTGGCGGTATGACTACTCATCGAAGAAAGATCGAATGTGAGAAAGACCGT 766

Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAenArgAsnPhleAsnSerIys 203
Db 767 TCTTTCTATGCGAAACAATCAITGTCATCGAAGACAGACCTGATAGAACTTTGCTTCCAAA 826

Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGGTGTAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTAT 886

Qy 224 ProGluSerGluProGluValIysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACACAGAGTGAAGCAGTGCCTAGTTCTTGAGAGAAATATCAACCCAG 946

Qy 244 IleIysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATACATCAGCATGCATTCATCTATCCAGCATATAGTGTTCCTATATTCCTAT 1006

Qy 264 ThrArgSerIysSerIysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACAGAAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTGCT 1066

Qy 284 AlaIleGluIysThrSerIysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAACCTAGTAAATATACAGGTATACATAGCCATGCGCTCAGAAACCTTA 1126

Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleIysTyrSerPhe 323
Db 1127 TACCTAGCTCCTGGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAATATTCGTTT 1186

Qy 324 -----ThrSerAs 326
Db 1187 ACAATTGAACCTCGAGATACGGGCACATACCGATTCTTGCTGCCGAGCGTTACATCAA 1246

Qy 326 nProProValGluIysLeuLeuProLeuSerLeuIys 338
Db 1247 CCCACCTGTAGAGAAGCTTTTGCCCGCTGCTCTCTCAA 1283

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RESULT 4

US-08-277-540-2

; Sequence 2, Application US/08277540

; Patent No. 5474901

; GENERAL INFORMATION:

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; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Alignment Scores:
Pred. No.: 6.58e-213 Length: 1749
Score: 1732.00 Matches: 338
Percent Similarity: 86.01% Conservative: 0
Best Local Similarity: 86.01% Mismatches: 0
Query Match: 96.33% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-3 (1-338) x US-08-277-540-2 (1-1749)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTCAAGAGTGCCCAAGTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAGATTCTA 166

Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuile 40
Db 167 CAGAACTCTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226

Qy 41 VallysIysIysGlnValHisPhePheValAsnAlaSerAspValAsnValIysAla 60
Db 227 GTGAAGAAAAACAAGTCCATTTTTTTGTAATGTCATGTCGACAAATGTGAAGCC 286

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuile 80
Db 287 CATTTAAATGTGAGCGGAATTCATGATGATGCTTGTGGCAGACGTGGAAGATCTTATT 346

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCAAACGACACACAGTACGCCCGAGCTCCGATCGTACTATGAACAG 406

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QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCAATAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGATCTCTGAT 466
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAAATTCACATTTGGATCTCTATTTGAGAGTACCCTCTATGTTTTAAAG 526
QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTCTGGAAAAGAACCAACGCCAAAATGCGATATGATGATGACTGTGGAATCCATGCC 586
QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAGAAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGGCCATATAACTCAATCTTAT 646
QY 175 ----- 175
Db 647 GGGATAATAGGCAATATACCAATCTCTGAGGCTTGTGATTTCTATGTTATGCGGTG 706
QY 176 -----AsnArgMetTrpArgLysAsnArg 183
Db 707 GTTAATGTGACGGTTTATCACTACTCATCGAAAAAGAAATCGAATGCGAGAAAGAACCGT 766
QY 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 767 TCTTTCTATGCGAACAATCATTTGCATCGGAACAGACCTGAATAGGAATTTTCTCTCCAAA 826
QY 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGTGTGAGGAAGTGCATCCAGTTCTCTATGCTCGGAACCTACTGTGACTTTAT 886
QY 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACCAAGAGTGAAGGCGAGTGGCTAGTTCTTGAGAGAAATATCAACAG 946
QY 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTAT 1006
QY 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACACGAAGTAAACGAAAGCCATGAGGAAGTCTCTCTAGTAGCCAGTGAAGCAGTTCTG 1066
QY 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAAATAGTAAATAATACAGGTATACATGCGCCATGGCTCAGAAACCTTA 1126
QY 304 TyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1127 TACCTAGCTCTCGAGGTGGGAGCATGATGATCTATGATTTGGGCATCAATAATTCGTT 1186
QY 324 -----ThrSerAs 326
Db 1187 ACAATTGAATTCAGATACGGGCACATACGGATTCTTGTGCGGAGCGTTACATCA 1246
QY 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1247 CCCACCTGTAGAGAAGCTTTTGGCGGTCTCTCTAAA 1283
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## RESULT 5

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US-08-430-787A-2
; Sequence 2, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-430-787A-2
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Alignment Scores:
Pred. No.: 6,58e-213 Length: 1749
Score: 1732.00 Matches: 338
Percent Similarity: 86.01% Conservative: 0
Best Local Similarity: 86.01% Mismatches: 0
Query Match: 96.33% Indels: 55
DB: 1 Gaps: 2
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US-09-980-881A-3 (1-338) x US-08-430-787A-2 (1-1749)
QY 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 107 TTTTCAGAGTGGCAAGTTCTAGCTGCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 166
QY 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 167 CAGAACTTTACTACAAATATGAGATTGTTCTCTGGCAGCCGTAACAGCTGACCTTATT 226
QY 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 227 GTGAGAAAAAACAAGTCCATTTTTTTGTAAATGTCATCTGATGTCACATGTGAAGGCC 286
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 287 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCCTTCTGGCAGACCGTGAAGATCTTATT 346
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 347 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCCGAGCCCTCCGATCTGCTACTATGACAG 405
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 407 TATCACTCAATAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGATCTCTGAT 466
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Qy 121 MetLeuThrLysIleHisGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 467 ATGCTTACAAATAATCCCATTTGGATTCCTCATTTGAGAAGTACCACCTCTATGTTTTAAAG 526
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 527 GTTCTGGAAGAACAACCAACGCAAAATGCCATATGATGTGACTGGGAATCCATGCC 586
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175
Db 587 AGAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAACTCAATTCTAT 646
Qy 175 ----- 175
Db 647 GGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCCGGTG 706
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183
Db 707 GTTAATGTGGACGGTTATGACTACTCATGGAAAGAAATCGAATGTGGAGAAGAACCGT 766
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 767 TCTTTCTATGGAACAATCATTTGATCGAAGACAGACCTGAATAGGAACCTTTGCTTCAAA 826
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 827 CACTGGTGTGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTAT 886
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 887 CCTGAGTCAGAACAGAGTGAAGCGAGTGGCTAGTTCTTGAGAAGAAATATCAACCAG 946
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 947 ATTAAGCATACATCAGCATGCTCATCTACTCCAGCATATAGTGTTCATATTCCTAT 1006
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 1007 ACAGAGTAAAGCAAGACCATGAGGAAGTCTCTTAGTAGCCAGTGAAGCAGTTGCT 1066
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1067 GCTATTGAGAAACTAGTAAATAATACCAGGTATACATGCGCATGCGTCAAGAACCTTA 1126
Qy 304 TyrLeuAlaProGlyGlyLysAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1127 TACCTAGCTCCTGAGGTGGGACGATGGATCTATGATTTGGGCATCAAAATATTCGTT 1186
Qy 324 -----ThrSerAs 326
Db 1187 ACAATTGAATTCAGATACGGGCACATACGATTTCTGTGCGGAGCGTTATATCAAA 1246
Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1247 CCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1283
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## RESULT 6

US-08-696-139-1  
; Sequence 1, Application US/08696139  
; Patent No. 5672496

## GENERAL INFORMATION:

; APPLICANT: Fayerman, Jeffrey T.  
; APPLICANT: Greenen, David P.  
; APPLICANT: Hershenberger, Charles L.  
; APPLICANT: Larson, Jeffrey L.  
; APPLICANT: Sterner, Jane L.  
; APPLICANT: Zhang, Haichao  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center

; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States of America  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696.139  
; FILING DATE:

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,258

FILING DATE: 16-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-8681

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756

TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1215 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1215

US-08-696-139-1

## Alignment Scores:

Pred. No.: 4,55e-73 Length: 1215  
Score: 646.50 Matches: 137  
Percent Similarity: 54.57% Conservative: 60  
Best Local Similarity: 37.95% Mismatches: 121  
Query Match: 35.96% Indels: 43  
DB: 1 Gaps: 6

US-09-980-881A-3 (1-338) x US-08-696-139-1 (1-1215)

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Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 28 TTCAGAGGGGAGAGGTGTTCCGTGTCATGTTGAAGATGAAATGACATCAGCTTACTC 87
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 88 CATGAGTTGGCCAGCACCGCAGGATTTGACTTCTTGGAAACCCAGATTCTGTCCACAAATC 147
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
Db 148 AAACCTCACAGTACAGTTGACTTCCGTGTGAAGACAGAGATATTTGGCTGTGGAAGAC 207
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 208 TTTCTGGAGCAGAAATGAATACAAATATGAGTACTCTATAAACACCTCGAGATCTGTGCTC 267
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 268 GAGGCTCAGTTTGACAGCAGATC-----CGTACAACTGGACACAGTTATGAGAAG 318
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 319 TACAACAACCTGGGAAACGATCGAGGCTTGGACTAAGCAAGTCACCACTGAAATCCAGAC 378
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 379 CTCATCTCTCGCACAGCCATCGGAACCTACATTTTATAGGAAACATATATATACCTCTCAAG 438
```

141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyLeuHisAla 160  
142 |||||  
143 GGT---GGCAACCTGGACCAATAGCTGCAATTTTCATGACTGGTTTCCATGCC 495  
144 |||||  
145 ArgGluTyrPheSerProAlaPheCysLeuTyrPhePhe 173  
146 |||||  
147 AGAAGATGGATTCCCATGCAATTTTCCAGTGGTTGTGAGAGAGCGCTGTTCTCACCTAT 555  
148 |||||  
149 --- 173  
150  
151 GGATATGAGAGTACATGACAGAAATTCCTCAACAGCTAGACTTTATGTCTGTGCTGTG 615  
152 |||||  
153 ---GlyHis 183  
154 |||||  
155 AsnArgMetTyrArgLysAsnArg 183  
156 |||||  
157 CTCATATTGATGGCTACATCTACACCTGGACCAACCGAATGTGGAGAAAGCCCGC 675  
158 |||||  
159 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
160 |||||  
161 TCTACCAATGCTGGAACCTACCTGCAATGGCACAGACCCCAACAGAAATTT---GATGCT 732  
162 |||||  
163 HisTyrCysGluGlyAlaSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
164 |||||  
165 GGTGGTGCAACACTGGAGCCCTACAGACCCCTGGATGAGACTTACTGTGGATCTGCT 792  
166 |||||  
167 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243  
168 |||||  
169 GCAGAGCTCTGAAAGAGACCAAGCCCTGGCTGATTTATAGGCACACCTCTCTCC 852  
170 |||||  
171 IleLysAlaTyrIleSerMetHisTyrSerGlnHisIleValPheProTyrSerTyr 263  
172 |||||  
173 ATCAAAGCATCTGACGATCCACTCATCTACAGATGATCTCTACCTTTATCTCTAT 912  
174 |||||  
175 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
176 |||||  
177 GATTACAAACTCTCCCGAGAACATGCTGAGTTGAATAACCTGGCTAAGCTGCCGTGAAA 972  
178 |||||  
179 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
180 |||||  
181 GAACIT---GCTACCTGTATGACACCAAGTACATACATGCGCCAGGAGCTACACATC 1029  
182 |||||  
183 TyrLeuAlaProGlyGlyAspTyrPheTyrAspLeuGlyIleLysTyrSerPhe 323  
184 |||||  
185 TATCCTGCTGCTGGGGCTCTGATGACTGGCTTATGACCAAGGAATCAATATTCCTTC 1089  
186 |||||  
187 Thr 324  
188 |||||  
189 ACC 1092

RESULT 7

US-08-860-882A-56  
Sequence 56, Application US/08860882A  
Patent No. 5985281  
GENERAL INFORMATION:  
APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
APPLICANT: EGGLETE, HENDRIKUS JOHANNES  
APPLICANT: TARRAGONA-FIOL, ANTONIO  
APPLICANT: RABIN, BRIAN ROBERT  
APPLICANT: BOYLE, FRANCIS THOMAS  
APPLICANT: HENNAM, JOHN FREDERICK  
APPLICANT: BLAKELY, DAVID CHARLES  
APPLICANT: MARSHAM, PETER ROBERT  
APPLICANT: HEATON, DAVID WILLIAM  
APPLICANT: DAVIES, DAVID HUW  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/860.882A  
FILING DATE: JUNE 23, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DONALD J. BIRD  
REGISTRATION NUMBER: 25,323  
REFERENCE/DOCKET NUMBER: 9901/238653  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3027  
TELEFAX: (202) 822-0944  
TELEX: 6174627 CUSH  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1263 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-860-882A-56  
Alignment Scores:  
Pred. No.: 7,07e-72 Length: 1263  
Score: 637.50 Matches: 130  
Percent Similarity: 54.85% Conservative: 68  
Best Local Similarity: 36.01% Mismatches: 120  
Query Match: 35.46% Indels: 43  
DB: 2 Gaps: 6  
US-09-980-881A-3 (1-338) x US-08-860-882A-56 (1-1263)  
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
142 |||||  
143 58 TTTGAAGCGCAGAGAGGTGTTCCGTGTTAAAGTGAAGATGAAAATCACAATAATCAT 117  
144 |||||  
145 21 GlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 40  
146 |||||  
147 118 CCGAGTGTGGCCAGCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTCACACAAATC 177  
148 |||||  
149 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
150 |||||  
151 178 AAACCTCACAGTACAGTTGACTTCGCTGTTAAAGCAGAGATGACTGTCTGCTGAGAAAT 237  
152 |||||  
153 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
154 |||||  
155 238 GTTCTAAAGCAGATGAACTACAAATACAAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 297  
156 |||||  
157 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
158 |||||  
159 298 GAGGCTCAGTTGATGAGCGGGTT-----CGTGCACACAGGACACAGATTATGAGAAG 348  
160 |||||  
161 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
162 |||||  
163 349 TACAACAGTGGGAAACGATAGAGGCTTGACTCAACAAGTCGCCACTGAGAATCCAGCC 408  
164 |||||  
165 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
166 |||||  
167 409 CTCATCTCTCGCAGTGTATATCGGAACCCACATTTTGAAGGGACGCGCTATTTACCTCTCCGAAG 468  
168 |||||  
169 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyIleHisAla 160  
170 |||||  
171 469 GTT---GGCAAGCTGGACCAAAATAGCCCTGCCATTTTCATGGACTGTGGTTTCCATGCC 525  
172 |||||  
173 161 ArgGluTyrPheSerProAlaPheCysLeuTyrPhePhe 173  
174 |||||  
175 526 AGAGAGTGGATTCTCTCTGCTATTCGCCAGTGGTTGTGTAAGAGAGAGGCTGTTCGTACCTAT 585  
176 |||||  
177 173 --- 173  
178 |||||  
179 586 GGACGTGAGATCAAGTGCAGAGAGCTTCTCGACACAGTTAGACTTTTATGTCTGCTGCTGTG 645

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Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183
Db 646 CTCATATGTGATGCTCATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 705
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 706 TCCACCATACCTGATCTAGCTGCTGATGGACACACCCCAACAGAAATTTT---GATGCT 762
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 763 GGTGGTGTGAATTTGGAGCCCTCTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 822
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 823 GCAGAGTCTGAAAGAGGACCAAGCCCTGGCTGATTTCAATCCGCAACAACTCTCTTCC 882
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 883 ATCAAGGCATATCTGACAAATCCATCTGTAATCCCAATGATGATCTACCTTACTCATAT 942
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 943 GCTTACAACTCGGTGAGAACAAATGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA 1002
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303
Db 1003 GAACCTT---GCCTCACTGACCGGACCAAGTACACATATGGCCCGGAGCTTACAAACAATC 1059
Qy 304 TyrLeuAlaProGlyGlyGlyAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1060 TATCTGCTGCTGGGGCTGTGACGACTGGCTTATGACCAAGGAATCAGATATTCCTTC 1119
Qy 324 Thr 324
Db 1120 ACC 1122

```

## RESULT 8

US-09-011-769A-38

Sequence 38, Application US/09011769A

Patent No. 6436691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKEY, David C.

DAVIES, David H.

HENNAM, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESS: Pillsbury Madison &amp; Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996  
 APPLICATION NUMBER: GB 9516810.0  
 FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1263 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-011-769A-38

Alignment Scores:

Pred. No.: 7,07e-72 Length: 1263

Score: 637.50 Matches: 130

Percent Similarity: 54.85% Conservative: 68

Best Local Similarity: 36.01% Mismatches: 120

Query Match: 35.46% Indels: 43

DB: 4 Gaps: 6

US-09-980-881A-3 (1-338) x US-09-011-769A-38 (1-1263)

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Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 58 TTTGAAGCGCAGAGGTGTTCCGTGTTAACGTTGAAGTGAATCAATTAACATAATC 117
Qy 21 GlnAsnLeuThrThrThrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40
Db 118 CGCAGATTGGCCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTGCACAAATC 177
Qy 41 VallysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60
Db 178 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAAGATACTGTCACGTGGAGAT 237
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 238 GTTCTAAAGCAGATGAATACATAAGGTACTGATAAGCAACCTGAGAAATGGTG 297
Qy 81 GlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 298 GAGGCTCAGTTTGATAGCCGGTT-----CGTCAACACAGCAGACAGTATATGAGAAG 348
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120
Db 349 TACAACAAAGTGGGAAACGATAGAGGCTTGACTCTACAAAGTCGCCACTGAGATCCAGCC 408
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 409 CTCATCTCTGCAGTGTATTATCGGAACCACTTTGAGGGAGCGGCTATTACTCTCTGAAG 468
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
Db 469 GTT---GCCAAAGCTGGACAAATAAGCTGCCATTTTCATGGACTGTGGTTTCCATGCC 525
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 526 AGAGAGTGGATTTCTCTGTCATTTCTCCAGTGGTTTGTAAAGAGAGGCTGTTCTGACCTAT 585
Qy 173 ----- 173
Db 586 GGACGTGAGATCCAAGTGACAGAGCTTCTCGCAAGTTAGACTTTTATGTCTCTGCTGTG 645
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183
Db 646 CTCATATGTGATGCTCATCTACACCTGGACCAAGAGCCGATTTTGGAGAAAGACTCGC 705
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 706 TCCACCATACCTGATCTAGCTGCTGATGGACACACCCCAACAGAAATTTT---GATGCT 762
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223

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Db 763 GGTGGTGTGAATGGAGCCTTCGAAACCCCTGTGATGAACCTTACTGTGGACCTGCC 822  
Qy 224 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 823 GCAGAGTCTGAAGAGAACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCC 882  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 883 ATCAGGCATATCTGCATCCACTCTGACTCTCCAAATGATGATCTACCTTACTCATAT 942  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 943 GCTTACAACTCGGTGAGAACCAATGCTGAGTTGAATGCCCTGCCTAAAGCTACTGTGAAA 1002  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1003 GAACCTT--GCCTCACTGCACCGCACCAAGTACACATATGGCCGGGAGCTACAACTATC 1059  
Qy 304 TyrLeuAlaProGlyGlyGlyAspTyrPheTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1060 TATCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1119  
Qy 324 Thr 324  
Db 1120 ACC 1122

RESULT 9

US-08-860-882A-71  
; Sequence 71, Application US/08860882A  
; Patent No. 5985281  
; GENERAL INFORMATION:  
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
; APPLICANT: EGGLESTE, HENDRIKUS JOHANNES  
; APPLICANT: TARRAGONA-FIOL, ANTONIO  
; APPLICANT: RABIN, BRIAN ROBERT  
; APPLICANT: BOYLE, FRANCIS THOMAS  
; APPLICANT: HENNAM, JOHN FREDERICK  
; APPLICANT: BLAKELY, DAVID CHARLES  
; APPLICANT: MARSHAM, PETER ROBERT  
; APPLICANT: HEATON, DAVID WILLIAM  
; APPLICANT: DAVIES, DAVID HOW  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860, 882A  
; FILING DATE: JUNE 23, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DONALD J. BIRD  
; REGISTRATION NUMBER: 25,323  
; REFERENCE/DOCKET NUMBER: 9901/238653  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3027  
; TELEFAX: (202) 822-0944  
; TELEX: 6174627 CUSH  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1284 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-860-882A-71  
Alignment Scores:  
Pred. No.: 7,27e-72 Length: 1284  
Score: 637.50 Matches: 130  
Percent Similarity: 54.85% Conservative: 68  
Best Local Similarity: 35.01% Mismatches: 120  
Query Match: 35.46% Indels: 43  
Gaps: 6  
DB: 2  
US-09-980-881A-3 (1-338) x US-08-860-882A-71 (1-1284)  
Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 85 TTTGAAGCGGAGAGGTGTTCCGTGTTAAAGTGAAGATGAAAAATCAATTAACATAATC 144  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuLeu 40  
Db 145 CCGGAGTTGGCCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTACACAATC 204  
Qy 41 ValLysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 205 AAACCTCACAGTACAGTTGACTTCGCTGTTAAAGCAGAAGATCTGCTCACTGTGAGAAT 264  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
Db 265 GTTCTAAAGCAGAAATGAATACATAACAAGGTACTGATAAGCAACCTGAGAAATGTGGTG 324  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 325 GAGGCTCAGTTGATAGCGGGTT-----CGTCAACAGGACACACAGTTTATGAGAAG 375  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 376 TACAACAAGTGGAAACCGATAGAGCTTGGACTCAACAAGTCGCCACTGAGAAATCCAGCC 435  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 436 CTCATCTCTCGCAGTGTATCGAAACACATTTGAGGGACGCGCTATTTACCTCTCTGAAG 495  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIleHisAla 160  
Db 496 GTT--GGCAAGCTGGACAAATAAGCTGCTTCATTTTCATGACTGTGGTTTCCATGCC 552  
Qy 161 ArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 173  
Db 553 AGAGAGTGGATTTCTCTGCTGCTTCTGCCAGTGGTTTGTAAAGAGAGGCTGTTCTGATCAT 612  
Qy 173 ----- 173  
Db 613 GCAGGTGAGATCCAAGTGACAGAGCTTCTCGACAAGTTAGACTTTTATGCTGCTGCTGTG 672  
Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183  
Db 673 CTCATATATTGATGGCTTACATCTACCTGGACAAGAGCCGATTTTGGAGAAAGACTCGC 732  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 733 TCACCCACTAGTGGATCTAGCTGATGGCACAGACCCCAACAGAAATTTT---GATGCT 789  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 790 GGTGGTGTGAAATTGGAGCCTCTCGAAACCCCTGTGATGAACTTACTGTGACCTGCC 849  
Qy 224 ProGluSerGluProGluValValAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 850 GCAGAGTCTGAAAGGAGAGACCAAGGCCCTGGCTGATTTTCATCCGCAACAACTCTCTTCC 909  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 910 ATCAAGGCATATCTGCAATCCACTGCTACTCCCAATATGATGATCTACCTTACTCATAT 969  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283







Db 1030 GAACCTT---GCCTCACTGACGGCACCAAGTACATATGCGCCGGGAGCTACACAAATC 1086  
 Qy 304 TyrLeuAlaProGlyGlyClyAspAspTrpIleTyrAspLeuGlyIleTyrSerPhe 323  
 Db 1087 TATCTGCTGCTGGGGCTCTGACAGCTGGGCTTATGACCAAGGAATCAGATATTCCTTC 1146  
 Qy 324 Thr 324  
 Db 1147 ACC 1149

RESULT 11  
 US-09-023-655-1020  
 ; Sequence 1020, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1020:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1622 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: g179933  
 ; US-09-023-655-1020

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 Query Match: 34.59% Indels: 44  
 DB: 4 Gaps: 7

US-09-980-881A-3 (1-338) x US-09-023-655-1020 (1-1622)

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Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeu 40  
 Db 121 AAGGACTTGGCCAAACCAATGAGCTTCTGGTATCCAGGTGCGCCACCACCCAGTA 180  
 Qy 41 VallyslylsGlnValHisPhePheValAsnAlaSerAspValAspAsnValValAla 60  
 Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAGGAATCCCAAGCCATCCAGTCT 240  
 Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
 Db 241 GCCTTGGATCAAAATAAATCCACTATGAAATCTTGATTCATGATCTACAAGAAGAGATT 300  
 Qy 81 GlnGlnIleSer---AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99  
 Db 301 GAGAAACAGTTTGATGTTAAAGAGATATCCAGCGAGGCACAGC-----TACGCA 351  
 Qy 100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119  
 Db 352 AAATACATAAATTCGGAAAGATTGGCTTGGACTGAAAGATGATGGATAAGTATCTCT 411  
 Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrTrpLeuValLeu 139  
 Db 412 GAAATGGTCTCTCGTATTAAATTTGGATCTACTGTTGAAGATAATCCACTATATGTTCTG 471  
 Qy 140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159  
 Db 472 AAGATT---GGGAAAGAAATGAAAGAAAGAGCTATTTTATGGATTGTGGCATTCAC 528  
 Qy 160 AlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173  
 Db 529 GCACGAGAATGGTCTCCCGCAGCATTTCTGCGAGTGTGTCTATCAGGCAACCAAACT 588  
 Qy 173 ----- 173  
 Db 589 TATGGGAAACAAATTTATGACCAAACTCTTGGACCAAGTGAATTTTACATTTCTCTCT 648  
 Qy 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182  
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 Db 766 GCTTCATGAACTCCATTCCTTAACCAATGACCAATGTCGAGATAACTATCGGGCTCT 825  
 Qy 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsn 242  
 Db 826 GCACCAGAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTTATTAGAAGCCACCTGAAT 885  
 Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262  
 Db 886 GAAATCAAGGTTTACATCACCCTTCCATTCCTACTCCAGATGCTATTGTTTCCCTATGGA 945  
 Qy 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282  
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 Qy 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302  
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 Db 1123 TTT 1125  
 RESULT 12

US-09-675-305-9  
; Sequence 9, Application US/09675305  
; Patent No. 6441153  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/675,305  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: US 60/156,685  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1311  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-09-675-305-9

Alignment Scores:  
Pred. No.: 1,596-69 Length: 1311  
Score: 619.50 Matches: 136  
Percent Similarity: 51.15% Conservatives: 64  
Best Local Similarity: 34.78% Mismatches: 127  
Query Match: 34.45% Indels: 64  
DB: 4 Gaps: 8

US-09-980-881A-3 (1-338) x US-09-675-305-9 (1-1311)

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Qy	41	ValLys-----LysLysGlnValHisPheValAsnAlaSerAspValAsnVal	58
Db	229	TCAGAGGGAACAGTACTGATGTCATATCCCCCAAAATGTTCCCGAGCC-----CTG	282
Qy	59	LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp	78
Db	283	TTAGCCTTCTTACAGAGGAGCAACATCCAGTACAAAGGTCTCATAGAGATCTTCAGAAA	342
Qy	79	LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSer-----	96
Db	343	ACACTGGAGAGGAGGAGCAGCTTGACACCCAGAGAAACCGAAGATCCCTCTCGGATAT	402
Qy	97	TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGlu	116
Db	403	AATTAGAGTTTATCACTCTCTTAGAGAAATTCAAAATTTGGATGCATCTCGAATAA	462
Qy	117	ArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeu	136
Db	463	ACTCACTCAGGCTCATTCACATGTTCTTATTTGAAGATCATATGAGGGAAGATCTCT	522
Qy	137	TyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCys	156
Db	523	TTTATTTTAAAGCTG---GGCAGAGCATCAACGACTCAAAAGAGCTGTTTGGATAGCTGT	579
Qy	157	GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle-----	173
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121	MetLeuThrIleHisIleGlySerSerPheGluLysIleValLeuTyrValLeuLys	140
415	CTCATCTCTCGCAGTGTATTACGGAACACCAATTTGAGGAGCGCGCTATTACCTCTCTGAAG	474
141	ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla	160
475	GTT---GGCAAAGCTGGACAAATAAGCTGCCATTTTCATGGAGCTGTGGTTTCCATGCC	531
161	ArgGlnTrpIleSerProAlaPheCysLeuTrpPheIle	173
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173	-----	173
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174	-----GlyHis-----AsnArgMetTrpArgLysAsnArg	183
652	CTCAATATTGATGGCTACATCTACACCTGGACCAAGAGCCGATTTTCGGAAGAAGACTCGC	711
184	SerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys	203
712	TCCACCATACTGGATCTAGCTGCATTTGGACACAGCCCAACAGAAATTTT---GATGCT	768
204	HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr	223
769	GGTTGGTGTGAATTTGGAGCCTCTCGAAACCCCTGTGATGAACTTACTGTGGACCTGCC	828
224	ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln	243
829	GCAGAGTCTGAAAGAGGAGACAAGGCCCTGGCTGATTTTCATCCGCACAAACTCTCTTC	888
244	IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr	263
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264	ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg	283
949	GCTTACAAACTCGGTGGAACAACTGCTGAGTTGAATGCCCTGGCTAAAGCTACTGTGAAA	1008
284	AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu	303
1009	GAACTT---GCCCTACCTGACGGCACCAGTACACATATGTCGCCGGAGCTTACAAACATC	1065
304	TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe	323
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US-08-782-760-5
; Sequence 5, Application US/08782760
; Patent No. 5948668
; GENERAL INFORMATION:
; APPLICANT: Hartman, Jacob
; APPLICANT: Fulga, Netta
; APPLICANT: Mendelovitch, Simona
; APPLICANT: Gorecki, Marian
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

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Thu Oct 28 07:16:14 2004

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Qy 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255
Db 535 TTCATCCGCAACAACCTCTCCACCATCAAGGCTACCTGACCATCCACTCATACTCACAG 594
Qy 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275
Db 595 ATGATGCTCTACCTTACTCTCTATGACTACAACTGCCTGAGAACTATGAGGAATTGAAT 654
Qy 276 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295
Db 655 GCCCTGGTGAAGGTGGCGCAAGGAGCTT---GCCACTCTGCTGATGGCACCACCAAGTACACA 711
Qy 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 315
Db 712 TATGCCCCAGGAGCTACACATCTATCTGCTGGGGGATCTGACGACTGGTCTTAT 771
Qy 316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 335
Db 772 GATCAGGGAATCAATATTCTTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830
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Search completed: October 27, 2004, 02:01:18  
Job time : 100.797 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 27, 2004, 01:54:23 ; Search time 1619.11 Seconds  
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Perfect score: 1798  
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Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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Alignment Scores:

Result No.	Score	Query Match	Length	DB ID	Description
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3	1732	96.3	1728	9	US-09-880-107-2396
4	1708.5	95.0	1344	16	US-10-115-479-69
5	1708.5	95.0	1743	16	US-10-115-479-67
6	1628	90.5	1272	15	US-10-379-836-1
7	1329.5	73.9	1037	16	US-10-115-479-63
8	1290.5	71.8	1132	16	US-10-115-479-65
9	902	50.2	1400	9	US-09-925-302-24
10	902	50.2	1400	10	US-09-925-302-24
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34	549	30.5	1870	9	US-09-910-059-112
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; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
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; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

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Query Match: 97.30% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-3 (1-338) x US-09-813-133A-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTTCAGAGTGCCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTTCTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 202

Qy 41 ValLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGCAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATTCATGCGAGTGTCTGTCGAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCAAACACACAGTCCAGCCCGGAGCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTAATCTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCACATTCATGCTCTTCTAGAACCTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGGAAGAACACAGACGCAAAATGCCATATGGATTGATGTGGAAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
Db 563 AGAAGATGGATCTCTCTGCTTTCTGCTTGGTTTCATAGGCCATATATCGAATGTGGAGA 622

Qy 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGTTCTTTCTATGCGAACCAATCATTTGTCATCGAACAGACCTGAATAGGAACCTTT 682

Qy 201 AlaSerLysHisTrpCysGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGGTGTGAGAGAGTGCAATCCAGTTCTCTATGCTCGGAACCTACTGT 742

Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 240  
Db 743 GGACTTTATCTCTAGTTCAGAACCGAGAGTGAAGCAGTGGCTAGTTCTTGTGAGAGAAAT 802

Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACAGATTAAAGCATACATCAGCATGCTATTCATCTCCAGCATATAGTGTCTTCCA 862

Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCTCTATACAGCAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAGTGAA 922

Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCTGTATTGAGAAAATTAAGTAAATACAGGATATACATATGGCCATGGCTCA 982

Qy 301 GluThrLeuTyrLeuAlaProGlyGlyCysAspTrpIleTyrAspLeuGlyIleLys 320  
Db 983 GAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATGGATCTATGATTTGGGCATCAAA 1042

Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCGTTTACAATGAACTTCGAGATACGGGCACATACGATTCCTGCTGCCGAGCGT 1102

Qy 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAAAACCCACCTGTAGAGAAGCTTTTGCCGCTGTCTCTAAAA 1148

RESULT 2  
US-10-212-877-1  
; Sequence 1, Application US/10212877  
; Publication No. US20030017574A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; FILE OF INVENTION: US/10212877  
; FILE OF INVENTION: US/10212877  
; FILE REFERENCE: CL001173DIV  
; CURRENT APPLICATION NUMBER: US/10/212,877  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-877-1

Alignment Scores:  
Pred. No.: 6,31e-206 Length: 1625  
Score: 1749.50 Matches: 336  
Percent Similarity: 94.38% Conservative: 0  
Best Local Similarity: 94.38% Mismatches: 2  
Query Match: 97.30% Indels: 18  
DB: 9 Gaps: 1

US-09-980-881A-3 (1-338) x US-10-212-877-1 (1-1625)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 83 TTTTCAGAGTGCCTAGTCTCTTCTAGAACCTCTAGGCAAGTTCAAGTTCTTA 142

Qy 21 GlnAsnLeuThrThrTyrGluLeuValLeuTrpGlnProValThrAlaAspLeu 40  
Db 143 CAGAACTTCTACTCAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 202

Qy 41 ValLysLysGlnValHisPheValAsnAlaSerAspValAspValLysAla 60  
Db 203 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGCAATGTGAAAGCC 262

Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeu 80  
Db 263 CATTTAAATGTGAGCGGAATTCATGCGAGTGTCTGTCGAGATGTGGAAGATCTTATT 322

Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 323 CAACAGCAGATTTTCCAAACACACAGTCCAGCCCGGAGCTCCGATCGTACTATGAACAG 382

Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 383 TATCACTCACTAAATGAATCTATTCTTGGATAGAAATTTAATCTGAGAGCATCTTGAT 442

Qy 121 MetLeuThrLysIleHisIleGlySerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 443 ATGCTTCAAAAAATCCACATTCATGCTCTTCTAGAACCTCTATGTTTAAAG 502

Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 503 GTTTCTGGAAGAACACAGACGCAAAATGCCATATGGATTGATGTGGAAATCCATGCC 562

Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180



Db 563 AGAGNATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCAATCGAATGGAGA 622  
Qy 181 LysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200  
Db 623 AAGAACCGTCTCTTATGCGAACAATCATTTGCATCGGAACAGACCTGAATAGGAACCTTT 682  
Qy 201 AlaSerLysHisTyrCysGluGluClyAlaSerSerSerCysSerGluThrTyrCys 220  
Db 683 GCTTCCAAACACTGTGTGTGAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGT 742  
Qy 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaLaserPheLeuArgAsn 240  
Db 743 GGACTTTATCTGAGTCAGAACCAAGAGTGAAGCGAGTGGCTAGTTCTTGAGAAGAAAT 802  
Qy 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
Db 803 ATCAACCAAGATTAAAGCATACATCAGCATGCATTCATATCCAGCATATAGTGTTCCTCA 862  
Qy 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
Db 863 TATTCCTATACAGAAAGTAAAGCAAGAACCAATGAGGAACCTGCTCTAGTAGCCAGTGA 922  
Qy 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300  
Db 923 GCAGTTCGTGCTATTGAGAAATATTAGTAAANATACCAGGTATACACATGGCCATGGCTCA 982  
Qy 301 GluThrLeuTyrLeuAlaProGlyGlyAspAspTyrIleTyrAspLeuGlyIleLys 320  
Db 983 GAAACCTTATACCTAGTCTCTCGAGGTGGGACGATTGGATCTATGATTTGGGCATCAA 1042  
Qy 321 TyrSerPhe----- 323  
Db 1043 TATTCGTTTACAAATTGAACTTCGAGATACGGGCACATACGGATTCTTGCTCCCGGAGCGT 1102  
Qy 324 -ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1103 TACATCAAAACCCACCTGTAGAGNAGCTTTTGGCGGTGCTCTTAA 1148

RESULT 3

US-09-880-107-2396  
: Sequence 2396, Application US/09880107  
: Patent No. US20020142981A1  
: GENERAL INFORMATION:  
: APPLICANT: Horne, Darci T.  
: APPLICANT: Vockley, Joseph G.  
: APPLICANT: Scherf, Uwe  
: APPLICANT: Gene Logic, Inc.  
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
: FILE REFERENCE: 44921-5028-WO  
: CURRENT APPLICATION NUMBER: US/09/880,107  
: CURRENT FILING DATE: 2001-06-14  
: PRIOR APPLICATION NUMBER: US 60/211,379  
: PRIOR FILING DATE: 2000-06-14  
: PRIOR APPLICATION NUMBER: US 60/237,054  
: PRIOR FILING DATE: 2000-10-02  
: NUMBER OF SEQ ID NOS: 3950  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 2396  
: LENGTH: 1728  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:

Pred. No.: 1,03e-203 Length: 1728  
Score: 1732.00 Matches: 338  
Conservative: 0  
Percent Similarity: 86.01% Mismatches: 0  
Best Local Similarity: 86.01% Indels: 55  
Query Match: 96.33% Gaps: 2  
DB:

US-09-980-881A-3 (1-338) x US-09-880-107-2396 (1-1728)  
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTTCAGAGTGGCCAAAGTTCTAGCTGCTCTTCTTGAACCTCTAGGCAAGTTCAAGTTCTA 145  
Qy 21 GlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 146 CAGAACTCTACTACAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 205  
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 206 GTGAAGAAAAAACAAAGTCCATTTTTTTGTAAATGCATCTGATGTGCGAATGTGAAAGCC 265  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 266 CATTTAAATGTGACGGGAATTCATGCACTGCTCTTGGCAGACGTTGGAAGATCTTATT 325  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 326 CAACAGCAGATTTCCAAACGACACAGTCAGCCCCCGAGCCTCCGCATCGTACTATGAACAG 385  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCACTAAATGAATCTATTCTTGGATAGAATTTATTAACCTGAGAGCATCCTGAT 445  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 446 ATGCTTCAAAAATCCACATTTGGATTCCTATTGAGAAGTACCCACTCTATGTTTAAAG 505  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 506 GTTTCGAAAGAAACAAACAGCCAAATGCCATATGATGATTTGACTGTGGAATCCATGCC 565  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175  
Db 566 AGAGAAATGGATCTCTCTGCTTCTGCTTGTGTTTCATAGGCCATATAAATCAATCTTAT 625  
Qy 175 ----- 175  
Db 626 GGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTATGTTATGCGGGTG 685  
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
Db 686 GTTAATGTGACGGTTATGACTACTCATGGAAGAAATCGAATCTGAGAAAGAACCTT 745  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 746 TCTTTCTATGGAACAATCAATTCATGTCGGAACAGACCTGGAATAGGAACCTTTGCTTCCAA 805  
Qy 204 HisTrpCysGluGluGluValSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 806 CACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGACCTTAT 865  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsnIleAsnGln 243  
Db 866 CTTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGTTCTTCTGAGAAGAAATATCAACAG 925  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 926 ATTTAAAGCATACATCAGCATGCATTCATACCTCCAGCATATAGTGTGTTCCATATTCCTAT 985  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 986 ACAGAAAGTAAAGCAAGACCATCAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGT 1045  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1046 GCTATTGAGAAACCTAGTAAANATACCAGGTATACACATGGCCATGGCTCAGAAACCTTA 1105  
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe 323



QY 259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278  
Db 997 TTTCCATATCTCTATACAGAGTAAAGCAAGCACTAGGAAGTCTCTAGTAGCC 1056  
QY 279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298  
Db 1057 AGTGAAGCAGTTCTGCTATTGAGAAAATTAGTAAATAATACCAGGTATACACATGGCCAT 1116  
QY 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly 318  
Db 1117 GCGTCAGAAACCTTATACCTAGCTCTCGAGGTGGGACGATTTGGATCTATGATTTGGC 1176  
QY 319 IleLysTyrSerPhe----- 323  
Db 1177 ATCAAAATATCTGTTTACAAATCGAATTCGAGATAGGGCACATACGGATTTCTGTGCGG 1236  
QY 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1237 GAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAAA 1288

## RESULT 5

US-10-115-479-67  
; Sequence 67, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytak, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glendda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 67  
; LENGTH: 1743  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20)..(1304)  
US-10-115-479-67  
Alignment Scores: 8.55e-201 Length: 1743  
Score: 1708.50 Matches: 336  
Percent Similarity: 84.42% Conservative: 0  
Best Local Similarity: 84.42% Mismatches: 2  
Query Match: 95.02% Indels: 60  
DB: 16 Gaps: 3  
US-09-980-881a-3 (1-338) x US-10-115-479-67 (1-1743)  
QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 86 TTTCCAGAGTGCCCAAGTTCTAGTCTCTCTCTAGAACCTCTAGGCAAGTTCAAGTTCTA 145  
QY 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 146 CAGAATCTTACTACAAACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTAT 205  
QY 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnVallyAla 60  
Db 206 GTGAAGAAAAACAAGTCCATTTTTTGTAAATGCAATCTGATGTGCACATGTGAAGCC 265  
QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValIleAspLeuIle 80  
Db 266 CATTTAATGTGAGCGGAATTCATGCAGTGTCTTGTGGCAGACGTGAAGATCTTAT 325  
QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 326 CAACAGCAGATTTCACACGACACAGTCAGCCCCCGAGCTCCGCATCGTACTATGAACAG 385  
QY 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 386 TATCACTCACTAAATGAATCTTATTTGGATAGAAATTTTATTAACCTGAGAGGCATCTGAT 445  
QY 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 446 ATGCTTACAAAATCCACATTCGATCTCTATTTGAGAGTACCCTCTATGTTTTAAAG 505  
QY 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155  
Db 506 GGTTCCTTTGAGCAGGTTTCTGAAAAAGAACAGCAAGCAAAATGCCATATGGATTGAC 565  
QY 156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 566 TGTGGAATCCATGCCAGAAATGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 625  
QY 175 ----- 175  
Db 626 ATAACCTCAATTCATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTTGTGGATTTC 685  
QY 176 -----AsnArgMet 178  
Db 686 TATGTTATGCCAGTGGTTAATGTGGATGGTTATGACTACTCTATCGAAAAAGAAATCGAATG 745  
QY 179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198  
Db 746 TGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCATCGGAACAGACCTGAATAGG 805

Qy 199 AsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThr 218  
Db 806 AACITTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCTCATGTCTGGAAACC 865  
Qy 219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 238  
Db 866 TACTGTGACATTTATCTCTGAGTCAGAACCCAGAGTGAAGGCGAGTGGCTAGTTCTTGAGA 925  
Qy 239 ArgSerLeuAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258  
Db 926 AGAAATATCAACAGATTAAAGCATACATACAGCATGCAATCCATCCACATATAGTG 985  
Qy 259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278  
Db 986 TTTCCATATTTCTATACAGCAAGTAAAGCAAGCAACCATGAGGACGTCTCTAGTAGCC 1045  
Qy 279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298  
Db 1046 AGTGAAGCAGTTCTGCTATTGAGAAATTTAGTAAATAATACAGGTATACATGGCCAT 1105  
Qy 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrIleTyrAspLeuGly 318  
Db 1106 GGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTATGATTTGGGC 1165  
Qy 319 IleLysTyrSerPhe----- 323  
Db 1166 ATCAAAATATCTTTACAAATTCGATTCGATACAGTACGGGACATACGATTTCTTCTGCCG 1225  
Qy 324 -----ThrSerAsnProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1226 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTGGCGGTCTCTTAAAA 1277

## RESULT 6

US-10-379-836-1  
; Sequence 1, Application US/10379836  
; Publication No. US20030215850A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BARBOON  
; TITLE OF INVENTION: TAFI  
; FILE REFERENCE: D0214NP  
; CURRENT APPLICATION NUMBER: US/10/379,836  
; CURRENT FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: U.S. 60/361,523  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Papio hamadryas  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1269)  
US-10-379-836-1

Alignment Scores:  
Pred. No.: 4,86e-191 Length: 1272  
Score: 1628.00 Matches: 318  
Percent Similarity: 83.21% Conservative: 9  
Best Local Similarity: 80.92% Mismatches: 11  
Query Match: 90.55% Indels: 55  
DB: 15 Gaps: 2

US-09-980-881A-3 (1-338) x US-10-379-836-1 (1-1272)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 67 TTTCCAGAGTGCCAGGTTCTAGCTGCTTCTTAGAACCTTAGCAAGTTCAAGTGCTA 126  
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeu 40  
Db 127 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCGGTAACAGCGGACCTTATT 186

Qy 41 VallysLysLysGlnValHisPheValAsnAlaSerAspValAspAsnValIleVal 60  
Db 187 GAGAAAGAAAGAAACCAAGTCCATTTTTTTGTAAATTCATCTGATGCGCAATGTGAAAGCC 246  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 247 CATTTAAATGTGAGCGGAATTCATGTCAGTGTCTCTGTCGACAGATGTGGAAGATCTTATT 306  
Qy 81 GlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 307 CAACAGCAGATTTCCAAACGACAGATGAGCCCGAGCCCTCCGATCCGTACTATGAACAG 366  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 367 TATCAGCTACATAAATGAATCTATTCTTGGATGAACTTATACTGAGAAGATCTTCGTAT 426  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 427 ATGCTTACAAAATCCACATTTGGATCTCTCATGAGAAGCACCACCTTTATGTTTTAAAG 486  
Qy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
Db 487 GTTTCTGGAAGAAACAAACAGCCAAATGCCATGTGGATTGACTGTGGAATCCATGCC 546  
Qy 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 175  
Db 547 AGAAGATGGATCTCCCTGCTTCTTCTGTGGTTTCATAGGCCATATACTGAATACTAC 606  
Qy 175 ----- 175  
Db 607 GGGATAATAGGGGAATATACCAATCTTCTGAGGCATGTGGATTTCTATGTTATGCCAGTG 666  
Qy 176 -----AsnArgMetTrpArgLysAsnArg 183  
Db 667 GTTAATGTGGATGGTTATGACTACTCATGGAAGAAATCGAATGTGAGAAAGAACCGT 726  
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203  
Db 727 TCTTTCTATCGGAACAATCGTTGATCGGAACAGACCTGAAACAGAACTTTTGGCTCAAA 786  
Qy 204 HisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223  
Db 787 CACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGCTCGGAAACCTACTGTGGACTTTAT 846  
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243  
Db 847 CCTGAGTCAGAACCCAGAAAGCGGCGTGGCTAAATTTCTTGAGAAGAAATATCAACAC 906  
Qy 244 IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263  
Db 907 ATTAAGCATACATCAGCATGCAATTCATCTCCAGCATATCGTGTTCATATTCCTAT 966  
Qy 264 ThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaValArg 283  
Db 967 ACTCGAAGCAAAAGCAAGACACAGAGGAATTTGTTCTAGTAGCCAGTGAAGCAGTTCTGT 1026  
Qy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeu 303  
Db 1027 GCTATTTCAGAAAAACCAAGTAAAAATATCAGGTATACATCGCGCTGGCTCAGAAACCTTA 1086  
Qy 304 TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe 323  
Db 1087 TACCTAGCTCTGGAGGTGGGACGATTTGATCTATGATTTGGGCATCAATATTCGTTT 1146  
Qy 324 -----ThrSerAs 326  
Db 1147 ACAATTGAACCTTCAGATACGGGCAAAATACGATTTCTTGCTGCTGACGCTTACATCAA 1206  
Qy 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338  
Db 1207 CCCACTTTGTAAGACGCGCTTTTGGCGGTGTCTCTAAAA 1243

RESULT 7  
 US-10-115-479-63  
 ; Sequence 63, Application US/10115479  
 ; Publication NO. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glendda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Malyanker, Uriel M.  
 ; APPLICANT: Shinkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
 ; CURRENT APPLICATION NUMBER: US/10/115,479  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,687  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; PRIOR APPLICATION NUMBER: 60/285,325  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SEQ ID NO 63  
 ; LENGTH: 1037  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (41)..(1007)  
 US-10-115-479-63  
 Alignment Scores:  
 Pred. No.: 3,48e-154  
 Score: 1329.50  
 Percent Similarity: 76.40%  
 Best Local Similarity: 76.40%  
 Query Match: 82

DB: 16 Gaps: 2  
 US-09-980-881A-3 (1-338) x US-10-115-479-63 (1-1037)  
 QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
 Db 107 TTT CAGAGTGCCCAAGTCTAGCTGCTCTCTAGAACCTCTAGCAAGTTCAAGTTCTA 166  
 QY 21 GlnAenLeuThrThrThrThrGluLeuValLeuTrpGlnProValThrAlaAspLeuLeu 40  
 Db 167 CAGAACTCTTACTACACATATGAGATTGTTCTCTGGCAGCCGGTAACAGCTGACCTTATT 226  
 QY 41 VallysLysLysGlnValHisPheValAenAlaSerAspValAspValAspValLysAla 60  
 Db 227 GTGAAGAAAAAACAAGTCCATTTTGTAAATGCATCTGATGTGCAACATGTGAAGCC 286  
 QY 61 HisLeuAenValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAspLeuLeu 80  
 Db 287 CATTTAAATGTGAGCGGAATTCATGCGAGTGTCTTCTGGCAGACGCTGGAGAGATCTTATT 346  
 QY 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTrpGluGln 100  
 Db 347 CAACAGCAGATTTCCACGACACACAGTCAGCCCCCGAGGCTCCGCATCTGCTACTATGAACAG 406  
 QY 101 TyrHisSerLeuAenGluLeuTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
 Db 407 TATCACTCACTAAATGAAATCTATTCTTGGATAGAAATTTATAACTGAGAGGATCTCTGAT 466  
 QY 121 MetLeuThrLysIleHisIleGlySerSerPheGlyLysTyrProLeuTyrValLeuLys 140  
 Db 467 ATGCTTACAAAAATCCACATCGATCCCTCATTTGAGAAGTACCCACTCTATGTTTAAAG 526  
 QY 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160  
 Db 527 GTTCTCGAAAAGAACACAGCGCCAAAATGCCATATGGATTGAC----- 571  
 QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180  
 Db 571 ----- 571  
 QY 181 LysAenArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAenArgAanPhe 200  
 Db 571 ----- 571  
 QY 201 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTyrCys 220  
 Db 572 -----TCT 574  
 QY 221 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAen 240  
 Db 575 GGACTTTTATCTCTAGTCAGAACAGAGTGAAGGAGTGGCTAGTTCTTTGAGAAGAAAT 634  
 QY 241 IleAenGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260  
 Db 635 ATCAACCAAGATTAAAGCATACATCAGCATGCACTCATACTCCAGCATATAGTGTTCCTCA 694  
 QY 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280  
 Db 695 TATCTCTATACAGAAAGTAAAGCAAGCAAGCCATGAGAACTGTCTCTAGTAGCCAGTGA 754  
 QY 281 AlaValArgAlaIleGluLysThrSerLysAenThrArgTyrThrHisGlyHisGlySer 300  
 Db 755 GCAGTTCGTGCTATTGAGAAAAATTAGTAAAAATACCAGGTATACATACATGCCATGCTCA 814  
 QY 301 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 320  
 Db 815 GAAACCTTATACCTAGCTCTCTGGAGTGGGAGCATGATTGATCTATGATTGGGCATCAAA 874  
 QY 321 TyrSerPhe----- 323  
 Db 875 TATTCGTTTACAACTTGAAGTACGGGCACATACGGATTCTTGTGCGGAGCGT 934  
 QY 324 -ThrSerAenProProValGluLysLeuLeuProLeuSerLeuLys 338

Db 935 TACATCAACCCACCTGTAGAGACCTTTTGGCGCTGCTCTATAA 980

RESULT 8

US-10-115-479-65

; Sequence 65, Application US/10115479

; Publication No. US20040006205A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Miller, Charles E.

; APPLICANT: Spitek, Kimberly A.

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Zhong, Haihong

; APPLICANT: Smithson, Glendda

; APPLICANT: Casman, Stacie J.

; APPLICANT: Boldog, Ferenc L.;

; APPLICANT: Voss, Edward

; APPLICANT: Vernet, Corine

; APPLICANT: MacDougall, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei

; APPLICANT: Mezes, Peter S.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Malyanker, Uriel M.

; APPLICANT: Shinkets, Richard A.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-322 B (Cura 622 PT)

; CURRENT APPLICATION NUMBER: US/10/115,479

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 60/281,136

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281,863

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/281,906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282,934

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283,657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,678

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,710

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/284,234

; PRIOR FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: 60/285,325

; PRIOR FILING DATE: 2001-04-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 198

; SEQ ID NO 65

; LENGTH: 1132

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (41)..(1103)

US-10-115-479-65

Alignment Scores:

Pred. No.: 2,74e-149 Length: 1132

Score: 1290.50 Matches: 263

Percent Similarity: 66.08% Conservative: 0  
Best Local Similarity: 66.08% Mismatches: 1  
Query Match: 71.77% Indels: 134  
DB: 16 Gaps: 4

US-09-980-881A-3 (1-338) x US-10-115-479-65 (1-1132)

Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20  
Db 107 TTTCCAGAGTGGCCCAAGTTCTAGCTGCTCTCTAGAACCTCTTAGCAAGTTCAAGTTCTA 166  
Qy 21 GlnAsnLeuThrThrThrGluValLeuTrpGlnProValThrAlaAspLeuIle 40  
Db 167 CAGAATCTTACTACAACATATGAGATTGTTCTCTGGCAGCGGTAAACAGCTGACCTTATT 226  
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60  
Db 227 GTGAAGAAAAACAAGTCCATTTTGTAAATGCATCTGATGTCGACAAATGTGAAAGCC 286  
Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80  
Db 287 CATTTAAATGTGAGCGGAATTCATGACAGTCTTGTGGCAGACGTGGAGAGATCTTATT 346  
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100  
Db 347 CAACAGCAGATTTCACACGACACAGTCAGCCCGAGSCCTCCGCATCTGTAATGAACAG 406  
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 120  
Db 407 TATCACTCACTAAATGAATCTATTCTTGGATGAATTTATACTGAGAGCATCTCTGAT 466  
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140  
Db 467 ATGCTTACAAAAATCCACATTTGGATCTCTATTGGAGAGTACCCTCTATGTTTTAAAG 526  
Qy 141 -----ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAsp 155  
Db 527 GGTTTCTTTGAGCAGGTTTCTGGAAAAAGAACAGCAGCCAAAAATGCCATATGATGATGAC 586  
Qy 156 CysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 175  
Db 587 TGTGGAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGTTGTGTTTCATAGGCCAT 646  
Qy 175 ----- 175  
Db 647 ATAACCTCAATCTATGGGATAATAGGCAATATACCAATCTCTCGAGGCTTGTGGATTTC 706  
Qy 176 -----AsnArgWet 178  
Db 707 TATGTTATGCGGTGGTTAATGTGATGTTATGACTACTCATGGAAAAAGATCGAATG 766  
Qy 179 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArg 198  
Db 767 TGGAGAAAGAACCCGTTCTTTCTATGCGAACAAATCATTCATCGAACAGACAGCCTGAATAGG 826  
Qy 199 AsnPheAlaSerLysHisTrpCysGluGluGluValaSerSerSerCysSerGluThr 218  
Db 827 AACTTTGCTTCCAAACACTGTTGTGAGAAAGGTGATCCAGTTCTCTCATGCTCGGAAACC 886  
Qy 219 TyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaLaserPheLeuArg 238  
Db 887 TACTGTGAGACTTTATCTCTGAG----- 907  
Qy 239 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 258  
Db 907 ----- 907  
Qy 259 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAla 278  
Db 907 ----- 907  
Qy 279 SerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHis 298

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Db 907 ----- 907
Qy 299 GlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGly 318
Db 908 ---TCAGAAACCTTATACCTAGCTCCTGGAGTGGGACGATTGATCTATGATTTGGC 964
Qy 319 IleLysTyrSerPhe----- 323
Db 965 ATCAATATTCGTTTACATTCGAACTTCGAGATCGGCACATACGGATTCTTGTCGCC 1024
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 1025 GAGCGTTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCTAAAA 1076

RESULT 9
US-09-925-302-24
; Sequence 24, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5,54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservativeness: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 9 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGTTGTTTATAGCCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCATGGGATAATAGGCAATATACCAATCTCTCGAGGCTTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCCGGTGTAAATGTGGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
Qy 179 pArgLysAsnArgSerPheTyrAlaIleHisCysIleGlyThrAspLeuAsnArgAs 199
Db 190 GAGAAAGAACCGTTCTTCTATCGAACAATCATTCGATCGGAACAGACCTGAATAGGAA 249
Qy 199 nPheAlaSerLysHisTrpCysGluGluAlaSerSerSerSerCysSerGluThrTy 219
Db 250 CTTTGTCTTCAAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTTA 309
Qy 219 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239
Db 310 CTGTGGACTTTTCTGAGTTCAGAACCCAGAAAGTGAAGGAGTGTAGTCTTCTTGAGAG 369
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Qy 239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259
Db 370 AAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTCCAGCATATAGTGT 429
Qy 259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279
Db 430 TCCATATTCCTATACACGAAGTAAAGCAAGACCATGAGAACTGTCTCTAGTAGCCAG 489
Qy 279 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 299
Db 490 TGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAATACCAAGTATACACATGCCATGG 549
Qy 299 ySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyI 319
Db 550 CTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGAGCATTTGGATCTATGATTTGGGCAT 609
Qy 319 eLysTyrSerPhe----- 323
Db 610 CAAATATTCGTTTACAAATTGAACTTCGAGATACGGGCACATACGGATTCTTGTGCCGGA 669
Qy 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338
Db 670 CGGTACATCAAAACCCACCTGTAGAGAAAGCTTTTGGCGTGTCTCTAAAA 719

RESULT 10
US-09-925-302-24
; Sequence 24, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 5,54e-101 Length: 1400
Score: 902.00 Matches: 181
Percent Similarity: 76.05% Conservativeness: 0
Best Local Similarity: 76.05% Mismatches: 1
Query Match: 50.17% Indels: 56
DB: 10 Gaps: 2

US-09-980-881A-3 (1-338) x US-09-925-302-24 (1-1400)
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Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 175
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGTTGTTTATAGCCCATATA 69
Qy 175 ----- 175
Db 70 ACTCAATTCATGGGATAATAGGCAATATACCAATCTCTCGAGGCTTGGATTCTAT 129
Qy 176 -----AsnArgMetTr 179
Db 130 GTTATGCCGGTGTAAATGTGGATGTTATGAACTACTCATGGAAGAAATCGAATGTG 189
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179 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 199  
 Db 190 GAGAAAGAACCGTTCTTTCTATGCAACAATCATTCGATCGCAACAGACCTGGAATAGGAA 249  
 199 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 219  
 Db 250 CTTTGCTTCCAAACACATCGTGTGAGGAAGGTGCATCCAGTTCTCTCATGCTCGGAACCTA 309  
 219 rCysGluLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 239  
 Db 310 CTGTGGACTTTATCTCGTGTGAGAACCAAGAGTGAAGGCAGTGGCTAGTTCTTTGAGAAG 369  
 239 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 259  
 Db 370 AAATATCAACAGATTAAAGCATCATCAGCATGCAITTCATCTCCAGCATATAGTGT 429  
 259 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 279  
 Db 430 TCCATATCTTATACAGAACTAAAGCAAGAACCATGAGGAATCTGTCTAGTAGCCAG 489  
 279 rGluAlaValAlaGlnIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGl 299  
 Db 490 TGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACCAAGGTATACACATGCCATGG 549  
 299 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIl 319  
 Db 550 CTCAGAACCTTATACCTAGTCTCTGGAGGTGGGGAGATGGATCTATGATTTGGGCAT 609  
 319 eLysTyrSerPhe----- 323  
 610 CAATATTCGTTTACAAATGGAATTCGAGATACGGGCACATACCGAATCTTGTGCGCGA 669  
 324 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 338  
 Db 670 GCGTTACATCAAAACCCACCTAGAGAAGCTTTTGGCGCTGCTCTATAAA 719

## RESULT 11

US-10-229-546-3  
 ; Sequence 3, Application US/10229546  
 ; Publication No. US20030082649A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weich, Nadine S.  
 ; APPLICANT: Carroll, Joseph M.  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: 6299, A HUMAN ZINC CARBOXYPEPTIDASE  
 ; FILE REFERENCE: MPT01-156P1RNM  
 ; CURRENT APPLICATION NUMBER: US/10/229,546  
 ; CURRENT FILING DATE: 2002-08-28  
 ; PRIOR APPLICATION NUMBER: 60/316,575  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1254  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1254)  
 US-10-229-546-3

Alignment Scores:  
 Pred. No.: 2,35e-66 Length: 1254  
 Score: 622.00 Matches: 128  
 Percent Similarity: 55.12% Conservative: 71  
 Best Local Similarity: 35.46% Mismatches: 118  
 Query Match: 34.59% Indels: 44  
 DB: 14 Gaps: 7

US-09-980-881A-3 (1-338) x US-10-229-546-3 (1-1254)

Qy 1 PheGlnSerGlyGlnValLeuAlaAlaLeuProArgThrSerArgGlnValGlnValLeu 20

Db 61 TTTGACAGGAGAGGTGTTCCGGTGAAGCCCGAGATGAAACACAGCAGCATCAT 120  
 Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaAspLeuIle 40  
 Db 121 AAGGACTTGGCCAAACCAATAGCTTCTGCTGATCCAGGTGCCACCCACCAAGTA 180  
 Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAsnValLysAla 60  
 Db 181 GCTGCTAATATGATGGTGGATTTCCGAGTTAGTGAGAAGGAATCCCAAGCCATCCAGTCT 240  
 Qy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaSerValGluAspLeuIle 80  
 Db 241 GCCTTGGATCAAAATAAAATGCACTATGAAATCTTGATTCATGATCTACAGAAGAGATT 300  
 Qy 81 GlnGlnGlnIleSer-----AsnAspThrValSerProArgAlaSerAlaSerTyrTyrGlu 99  
 Db 301 GAGAAACAGTTTGATGTTAAAGAAAGATATCCAGGCGAGGCACAGC-----TACGCA 351  
 Qy 100 GlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisPro 119  
 Db 352 AAATACATAAATTTGGGAAAAGATTGGCTTGGACTGAAAAGATGATGGATAAGTATCCT 411  
 Qy 120 AspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeu 139  
 Db 412 GAAATGCTCTCGTATTAAATTTGAACTTACTTGTGTAAGATTAATCCACTATATGTTCTG 471  
 Qy 140 LysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHis 159  
 Db 472 AAGATT--GGGAAAAGAAATGAAAGAAAGAGCTATTTTATGGATTGTGGCATTAC 528  
 Qy 160 AlaArgGluTrpLysSerProAlaPheCysLeuTrpPheIle----- 173  
 Db 529 GCACGAGAAATGGGTCTCCCGAGCATTTGCCAGTGTGCTGCTATCATCAGGCAACCAAACT 588  
 Qy 173 ----- 173  
 589 TATGGGGAACAAATAATATGACCAAACTCTTGGACCGAATGAATTTTACATTTCTCCT 648  
 174 -----GlyHis-----AsnArgMetTrpArgLysAsn 182  
 649 GTGTTCAATGTTGATGGATATATTTGGTTCATGACAAAGAACCGCATGTGAGAAAAAT 708  
 183 ArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSer 202  
 Db 709 CGTTCCAAGAACCAAACTCCAAATGCATCGCACTGACCTCAACAGGAATTTT---AAT 765  
 Qy 203 LysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeu 222  
 Db 766 GCTTCATGGAACTCCATTCCTTAACCAACCAATGACCCATGTCAGATTAATTCGGGGTCT 825  
 223 TyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsn 242  
 Db 826 GCACCAAGTCCGAGAAAGAGACGAAAGCTGTCACTAATTTTATTAGAACCCACCTGAAT 885  
 Qy 243 GlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSer 262  
 Db 886 GAAATCAAGGTTTTACATCACCTTCCATTCCTACTCCAGATGCTATTGTTTCCCTATGGA 945  
 Qy 263 TyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGluAlaVal 282  
 Db 946 TATACATCAAACTGCCACCTAACCATGAGACTTGGCCAAAGTTGCAAGATGGCACT 1005  
 Qy 283 ArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGluThr 302  
 Db 1006 GATGTTCTA---TCAACTCGATATGAACCCCGCTACATCTATGCCCCAATAGAATCAACA 1062  
 Qy 303 LeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSer 322  
 Db 1063 ATTTACCCGATATCAGGTTCTTCTTAGACTGGGCTTATGACCTGGGCATCAACACACA 1122  
 323 Phe 323  
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[illegible]

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OM protein - protein search, using sw model

Run on: October 27, 2004, 01:31:47 ; Search time 13.2903 Seconds  
(without alignment)  
1227.533 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 246  
Sequence: 1 ASASYEQVHSLNEIYSWIE.....IKSFTSPNPVVKLLPLSLK 246

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/prodata/1/iaa/PTUS\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	149	60.6	423	1	US-07-649-591B-3
2	149	60.6	423	1	US-08-277-540-3
3	149	60.6	423	1	US-08-430-787A-3
4	149	60.6	423	2	US-08-869-057-2
5	140	56.9	386	4	US-09-813-133A-2
6	112	45.5	423	4	US-09-813-133A-4
7	15	6.1	417	1	US-07-649-591B-7
8	15	6.1	417	1	US-08-277-540-7
9	15	6.1	417	1	US-08-430-787A-7
10	12	4.9	247	4	US-09-675-305-6
11	12	4.9	247	4	US-10-200-344-6
12	12	4.9	350	4	US-09-675-305-12
13	12	4.9	350	4	US-10-200-344-12
14	12	4.9	437	4	US-09-675-305-10
15	12	4.9	437	4	US-10-200-344-10
16	11	4.5	86	4	US-09-270-767-56648
17	11	4.5	89	4	US-09-513-999C-7648
18	11	4.5	216	4	US-09-270-767-41427
19	11	4.5	307	2	US-08-782-760-6
20	11	4.5	307	5	PCT-US96-00995-6
21	11	4.5	329	4	US-09-011-769A-51
22	11	4.5	349	4	US-09-011-769A-47
23	11	4.5	349	4	US-09-011-769A-60
24	11	4.5	349	4	US-09-011-769A-64
25	11	4.5	396	1	US-07-649-591B-4
26	11	4.5	396	1	US-08-277-540-4
27	11	4.5	396	1	US-08-430-787A-4

28	11	4.5	415	2	US-08-860-882A-57	Sequence 57, Appl
29	11	4.5	415	4	US-09-011-769A-39	Sequence 39, Appl
30	11	4.5	424	4	US-09-011-769A-56	Sequence 56, Appl
31	11	4.5	613	3	US-09-171-945-113	Sequence 113, App
32	11	4.5	716	3	US-09-171-945-125	Sequence 125, App
33	10	4.1	417	1	US-07-649-591B-6	Sequence 6, Appl
34	10	4.1	417	1	US-08-277-540-6	Sequence 6, Appl
35	10	4.1	417	1	US-08-430-787A-6	Sequence 6, Appl
36	10	4.1	417	4	US-09-513-999C-4204	Sequence 4204, Ap
37	9	3.7	162	4	US-09-248-796A-14973	Sequence 14973, A
38	9	3.7	417	1	US-07-649-591B-8	Sequence 8, Appl
39	9	3.7	417	1	US-08-277-540-8	Sequence 8, Appl
40	9	3.7	417	1	US-08-430-787A-8	Sequence 8, Appl
41	7	2.8	130	4	US-09-270-767-57790	Sequence 57790, A
42	7	2.8	171	4	US-09-248-796A-22616	Sequence 22616, A
43	7	2.8	184	4	US-09-513-999C-4204	Sequence 4204, Ap
44	7	2.8	219	2	US-08-925-708-2	Sequence 2, Appl
45	7	2.8	249	4	US-09-252-991A-30320	Sequence 30320, A

ALIGNMENTS

RESULT 1  
US-07-649-591B-3  
; Sequence 3, Application US/07649591B  
; Patent No. 5206161  
; GENERAL INFORMATION:  
; APPLICANT: Dennis Drayna and Daniel Eaton Carboxypeptidase  
; TITLE OF INVENTION: No. 5206161 Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/649,591B  
FILING DATE: 19910201  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear

US-07-649-591B-3

Query Match 60.6%; Score 149; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.8e-142;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 NRMWRKNRIFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 143  
DB 235 NRMWRKNRIFYANNHCIGTDLNRNFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 294



APPLICANT: Morser, Michael J  
APPLICANT: Nagahima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE: Plasma  
TISSUE TYPE: Plasma  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 23..401  
US-08-869-057-2

Query Match 60.6%; Score 149; DB 2; Length 423;  
Best Local Similarity 100.0%; Pred. No. 9.8e-142;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 294  
QY 144 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203  
Db 295 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 354  
QY 204 HGHGSETLYLAPCGDDWIYDLGKYSFT 232  
Db 355 HGHGSETLYLAPCGDDWIYDLGKYSFT 383

RESULT 5  
US-09-813-133A-2  
Sequence 2, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinui et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 2  
LENGTH: 386  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-2  
Query Match 56.9%; Score 140; DB 4; Length 386;  
Best Local Similarity 100.0%; Pred. No. 1e-132;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 AKNAIWDICGTHAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNRFASKHWC 115  
Db 170 AKNAIWDICGTHAREWISPAFLWFIHNRWNRKRSFYANNHCIGTDLNRFASKHWC 229  
QY 116 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHIHVPYSTRSK 175  
Db 230 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHIHVPYSTRSK 289  
QY 176 SKDHEELSLVASEAVRAIEK 195  
Db 290 SKDHEELSLVASEAVRAIEK 309  
RESULT 6  
US-09-813-133A-4  
Sequence 4, Application US/09813133A  
Patent No. 6455294  
GENERAL INFORMATION:  
APPLICANT: GAN, Weinui et al  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL001173  
CURRENT APPLICATION NUMBER: US/09/813,133A  
CURRENT FILING DATE: 2001-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Fast-SEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 423  
TYPE: PRT  
ORGANISM: Human  
US-09-813-133A-4

Query Match 45.5%; Score 112; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.8e-104;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 143  
Db 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCBEAGSSSCSETYCGLYPESEPEVKAVAS 294  
QY 144 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSDHEELSLVASEAVRAIEK 195  
Db 295 FLRRNINQIKAYISMHSYQHIHVPYSTRSKSDHEELSLVASEAVRAIEK 346

RESULT 7  
US-07-649-591B-7  
Sequence 7, Application US/07649591B  
Patent No. 5206161  
GENERAL INFORMATION:  
APPLICANT: Dennis Drayna and Daniel Eaton  
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/649,591B  
; FILING DATE: 19910201  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/266-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-649-591B-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 63 DCGIHAREWISPAFC 77  
Db 172 DCGIHAREWISPAFC 186

RESULT 8  
US-08-277-540-7  
; Sequence 7, Application US/08277540  
; Patent No. 5474901  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,540  
; FILING DATE: 19-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 01-FEB-91  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-277-540-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 63 DCGIHAREWISPAFC 77  
Db 172 DCGIHAREWISPAFC 186

RESULT 9  
US-08-430-787A-7  
; Sequence 7, Application US/08430787A  
; Patent No. 5593674  
; GENERAL INFORMATION:  
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,787A  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,540  
; FILING DATE: 19-JUL-1994  
; APPLICATION NUMBER: 08/167727  
; FILING DATE: 15-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/959944  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/649591  
; FILING DATE: 01-FEB-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 689D1C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-430-787A-7

Query Match 6.1%; Score 15; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 8.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 63 DCGIHAREWISPAFC 77



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Db      172 DCGIHAREWISPAFC 186
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RESULT 10
US-09-675-305-6
; Sequence 6, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-6

Query Match      4.9%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
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Db      190 WIDCGIHAREWI 201

RESULT 11
US-10-200-344-6
; Sequence 6, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 247
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-6

Query Match      4.9%; Score 12; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
|||||
Db      190 WIDCGIHAREWI 201

RESULT 12
US-10-200-344-12
; Sequence 12, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-12

Query Match      4.9%; Score 12; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
|||||
Db      190 WIDCGIHAREWI 201

RESULT 13
US-10-200-344-12
; Sequence 12, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 350
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-12

Query Match      4.9%; Score 12; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
|||||
Db      190 WIDCGIHAREWI 201

RESULT 14
US-09-675-305-10
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; Sequence 10, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-675-305-10
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Query Match 4.9%; Score 12; DB 4; Length 437;
Best Local Similarity 100.0%; Pred.No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 WIDCGIHAREWI 72
Db 190 WIDCGIHAREWI 201
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RESULT 15
US-10-200-344-10
; Sequence 10, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-200-344-10
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Query Match 4.9%; Score 12; DB 4; Length 437;
Best Local Similarity 100.0%; Pred.No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 WIDCGIHAREWI 72
Db 190 WIDCGIHAREWI 201
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Search completed: October 27, 2004, 01:53:59  
Job time : 14.2903 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 01:41:12 ; Search time 32.3136 Seconds  
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Title: US-09-980-881A-4  
Perfect score: 246  
Sequence: 1 ASASYEQVHSLNEIYSWIE.....IKYFSTNPPVKLLPLSLK 246

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1364641 seqs, 323758627 residues

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Minimum DB seq length: 0  
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- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	60.6	211	9	US-09-925-302-467
2	149	60.6	211	10	US-09-925-302-467
3	149	60.6	423	14	US-10-379-836-17
4	140	56.9	386	9	US-09-813-133A-2
5	140	56.9	386	14	US-10-212-877-2
6	112	45.5	423	9	US-09-813-133A-4
7	112	45.5	423	14	US-10-212-877-4
8	112	45.5	428	15	US-10-115-479-68
9	112	45.5	428	15	US-10-115-479-70
10	68	27.6	322	15	US-10-115-479-64
11	52	21.1	354	15	US-10-115-479-66
12	42	17.1	423	14	US-10-379-836-2
13	26	10.6	422	14	US-10-379-836-16

14	26	10.6	422	14	US-10-379-836-18	Sequence 18, Appl
15	12	4.9	210	16	US-10-363-829-401	Sequence 401, App
16	12	4.9	247	13	US-10-200-344-6	Sequence 6, Appli
17	12	4.9	315	9	US-09-888-615-60	Sequence 60, Appl
18	12	4.9	350	13	US-10-200-344-12	Sequence 12, Appl
19	12	4.9	434	16	US-10-477-515-2	Sequence 2, Appli
20	12	4.9	437	13	US-10-200-344-10	Sequence 10, Appl
21	12	4.9	437	14	US-10-274-639-12	Sequence 12, Appl
22	12	4.9	437	15	US-10-333-574-12	Sequence 12, Appl
23	12	4.9	437	17	US-10-757-262-128	Sequence 128, App
24	11	4.5	118	15	US-10-074-978A-274	Sequence 274, App
25	11	4.5	231	15	US-10-074-978A-48	Sequence 48, Appl
26	11	4.5	231	15	US-10-074-978A-50	Sequence 50, Appl
27	11	4.5	231	15	US-10-074-978A-52	Sequence 52, Appl
28	11	4.5	349	15	US-10-074-978A-46	Sequence 46, Appl
29	11	4.5	402	14	US-10-379-836-20	Sequence 20, Appl
30	11	4.5	416	15	US-10-074-978A-266	Sequence 266, App
31	11	4.5	417	15	US-10-074-978A-267	Sequence 267, App
32	11	4.5	417	15	US-10-074-978A-268	Sequence 268, App
33	11	4.5	417	16	US-10-477-515-3	Sequence 3, Appli
34	11	4.5	613	9	US-09-910-059-113	Sequence 113, App
35	11	4.5	613	16	US-10-608-710-4	Sequence 4, Appli
36	11	4.5	716	9	US-09-910-059-125	Sequence 125, App
37	10	4.1	180	14	US-10-106-698-6143	Sequence 6143, Ap
38	10	4.1	231	15	US-10-074-978A-54	Sequence 54, Appl
39	10	4.1	286	16	US-10-408-765A-1959	Sequence 1959, Ap
40	10	4.1	310	16	US-10-470-390A-20	Sequence 20, Appl
41	10	4.1	374	9	US-09-888-615-61	Sequence 61, Appl
42	10	4.1	416	15	US-10-074-978A-270	Sequence 270, App
43	10	4.1	417	14	US-10-229-546-2	Sequence 2, Appli
44	10	4.1	417	14	US-10-229-546-9	Sequence 9, Appli
45	10	4.1	417	14	US-10-341-434-188	Sequence 188, App

ALIGNMENTS

RESULT 1  
US-09-925-302-467  
; Sequence 467, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 467  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-302-467

Query Match 60.6%; Score 149; DB 9; Length 211;  
Best Local Similarity 100.0%; Pred. No. 5.8e-135;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	84	NRMWRKNRSFYANNHICIGTDLNPNFASKHWCSESSSSCSTYCGLYPESEPEVKAVAS	143
DB	23	NRMWRKNRSFYANNHICIGTDLNPNFASKHWCSESSSSCSTYCGLYPESEPEVKAVAS	82
QY	144	FLRRNINQIKATISHMHSYSQHIVFPYSTRSKDHEELSLVASEAVRAIEKTSKNTRYT	203
DB	83	FLRRNINQIKATISHMHSYSQHIVFPYSTRSKDHEELSLVASEAVRAIEKTSKNTRYT	142
QY	204	HGHGSETLLYAPGGDDMIYDLGIKYSFT	232

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Db      143 HGHGSETLYLAPGGDDWIYDLGIKYSFT 171
RESULT 2
US-09-925-302-467
; Sequence 467, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925.302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCR/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-467
Query Match      60.6%; Score 149; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 5.8e-135;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      84 NRMWRKNSFYANNHCIGTDLNRNPFASKHWCHEEGASSSSCSETYCGLYPESEPEVKAVAS 143
Db      23 NRMWRKNSFYANNHCIGTDLNRNPFASKHWCHEEGASSSSCSETYCGLYPESEPEVKAVAS 82
Qy      144 FLRRNINQIKAYISMHSYQHVFPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203
Db      83 FLRRNINQIKAYISMHSYQHVFPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 142
Qy      204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db      143 HGHGSETLYLAPGGDDWIYDLGIKYSFT 171
RESULT 3
US-10-379-836-17
; Sequence 17, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379.836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 17
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-836-17
Query Match      60.6%; Score 149; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1e-134;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      84 NRMWRKNSFYANNHCIGTDLNRNPFASKHWCHEEGASSSSCSETYCGLYPESEPEVKAVAS 143
Db      235 NRMWRKNSFYANNHCIGTDLNRNPFASKHWCHEEGASSSSCSETYCGLYPESEPEVKAVAS 294
Qy      144 FLRRNINQIKAYISMHSYQHVFPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203
Db      170 AKNAIWDCGHHAREWISPAFCLWFIHGRNMRKNSFYANNHCIGTDLNRNPFASKHWC 229

Db      295 FLRRNINQIKAYISMHSYQHVFPYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 354
Qy      204 HGHGSETLYLAPGGDDWIYDLGIKYSFT 232
Db      355 HGHGSETLYLAPGGDDWIYDLGIKYSFT 383
RESULT 4
US-09-813-133A-2
; Sequence 2, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813.133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-813-133A-2
Query Match      56.9%; Score 140; DB 9; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      56 AKNAIWDCGHHAREWISPAFCLWFIHGRNMRKNSFYANNHCIGTDLNRNPFASKHWC 115
Db      170 AKNAIWDCGHHAREWISPAFCLWFIHGRNMRKNSFYANNHCIGTDLNRNPFASKHWC 229
Qy      116 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHVFPYSTRSK 175
Db      230 EGASSSSCSETYCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYQHVFPYSTRSK 289
Qy      176 SKDHEELSLVASEAVRAIEK 195
Db      290 SKDHEELSLVASEAVRAIEK 309
RESULT 5
US-10-212-877-2
; Sequence 2, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212.877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-877-2
Query Match      56.9%; Score 140; DB 14; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4e-126;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      56 AKNAIWDCGHHAREWISPAFCLWFIHGRNMRKNSFYANNHCIGTDLNRNPFASKHWC 115
Db      170 AKNAIWDCGHHAREWISPAFCLWFIHGRNMRKNSFYANNHCIGTDLNRNPFASKHWC 229
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84	Qy	NMWRNRPSFYANNHICIGTDLNRNPFASKHWCBEAGSSSSCSETYCGIYPSEPEVKAVAS	143
240	Db	NMWRNRPSFYANNHICIGTDLNRNPFASKHWCBEAGSSSSCSETYCGIYPSEPEVKAVAS	299
144	Qy	FLRRNINQIKAYISMHSYQSHIVFPYPSYTRSKSKDHBEELSLVASEAVRAJEK	195
300	Db	FLRRNINQIKAYISMHSYQSHIVFPYPSYTRSKSKDHBEELSLVASEAVRAJEK	351

## RESULT 9

US-10-115-479-70  
; Sequence 70, Application US/10115479  
; Publication No. US20040006205A1

	Query Match	45.5%;	Score 112;	DB 15;	Length 428;
	Best Local Similarity	100.0%;	Pred. No. 4.3e-99;		
	Matches 112;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
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Db	240	NRWRKRSFYANNHICGTDLNRNFASKHWC	EGASSSCSETYCGLYP	SEPEVKAVAS	299
Qy	144	FLRRNINQIKAYISMHSYOHIVPPYSYTR	SKSDHEELSLVASEA	VRATEK	195
Db	300	FLRRNINQIKAYISMHSYOHIVPPYSYTR	SKSDHEELSLVASEA	VRATEK	351

RESULT 10

US-10-115-479-64  
; Sequence 64, Application US/10115479  
; Publication No. US20040006205A1

REFFICANT: MAGAL, AMI  
: TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES. NUCLEIC ACIDS ENCODING SAME. AND METHOD

FILE OF INVENTOR: ANGELO RICCI  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18

; PRIORITY APPLICATION NUMBER: 60/281,136  
 ;  
 ; PRIORITY FILING DATE: 2001-04-03  
 ;  
 ; PRIORITY APPLICATION NUMBER: 60/281,863

;  
 ; PRIOR FILING DATE: 2001-04-05  
 ;  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ;  
 ; PRIOR FILING DATE: 2001-04-05  
 ;

; PRIOR APPLICATION NUMBER: 60/282,934  
 ;  
 ; PRIOR FILING DATE: 2001-04-10  
 ;  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ;

; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687  
 ;  
 ; PRIOR FILING DATE: 2001-04-13  
 ;  
 ; PRIOR APPLICATION NUMBER: 60/283,710

; PRIORITY FILING DATE: 2001-04-13  
; PRIORITY APPLICATION NUMBER: 60/284,234  
; PRIORITY FILING DATE: 2001-04-17

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; PRIOR APPLICATION NUMBER: 60/285,325
;
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data remains

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; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 70
; LENGTH: 428

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-70

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QY 57 KNAIWIDCGIHAREWISPAFCLWFIG 82

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|||||
Db      170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 14
US-10-379-836-18
; Sequence 18, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: D0214NP
; CURRENT APPLICATION NUMBER: US/10/379,836
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-836-18

Query Match      10.6%; Score 26; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      57 KNAIWIDCGIHAREWISPAFLWFIG 82
Db      170 KNAIWIDCGIHAREWISPAFLWFIG 195

RESULT 15
US-10-363-829-401
; Sequence 401, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 401
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:366783.1.orf1:2000SEP08
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 102
; OTHER INFORMATION: unknown or other
US-10-363-829-401

Query Match      4.9%; Score 12; DB 16; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 WIDCGIHAREWI 72
Db      48 WIDCGIHAREWI 59

Search completed: October 27, 2004, 01:56:33
Job time : 32.3136 secs
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GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:56:38 ; Search time 64.6271 Seconds  
(without alignments)  
2705.593 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues  
Word size: 1

Total number of hits satisfying chosen parameters: 1643622

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Database : Issued Patents NA:  
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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	149	60.6	1272	2	US-08-869-057-1 Sequence 1, Appli
2	149	60.6	1749	1	US-07-649-591B-2 Sequence 2, Appli
3	149	60.6	1749	1	US-08-277-540-2 Sequence 2, Appli
4	149	60.6	1749	1	US-08-430-787A-2 Sequence 1, Appli
5	140	56.9	1625	4	US-09-813-133A-1 Sequence 3, Appli
6	68	27.6	55827	4	US-09-813-133A-3 Sequence 5, Appli
7	12	4.9	741	4	US-09-675-305-5 Sequence 5, Appli
8	12	4.9	741	4	US-10-200-344-5 Sequence 11, Appl
9	12	4.9	1050	4	US-09-675-305-11 Sequence 11, Appl
10	12	4.9	1050	4	US-10-200-344-11 Sequence 9, Appli
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13	12	4.9	2128	4	US-09-675-305-13 Sequence 13, Appl
14	12	4.9	2128	4	US-10-200-344-13 Sequence 13, Appl
15	11	4.5	258	4	US-09-270-767-25119 Sequence 25119, A
16	11	4.5	359	4	US-09-513-999C-3571 Sequence 3571, Ap
17	11	4.5	927	2	US-08-782-760-5 Sequence 5, Appli
18	11	4.5	927	5	PCT-US96-00995-5 Sequence 5, Appli
19	11	4.5	999	2	US-08-860-882A-67 Sequence 67, Appl
20	11	4.5	999	4	US-09-011-769A-50 Sequence 50, Appl
21	11	4.5	1053	2	US-08-860-882A-64 Sequence 64, Appl
22	11	4.5	1053	4	US-09-011-769A-56 Sequence 46, Appl
23	11	4.5	1053	4	US-09-463-451-27 Sequence 27, Appl
24	11	4.5	1053	4	US-09-463-451-28 Sequence 28, Appl
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26	11	4.5	1059	2	US-08-860-882A-77 Sequence 77, Appl
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35	11	4.5	2154	3	US-09-171-945-124 Sequence 124, App
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37	9	3.7	486	4	US-09-248-796A-870 Sequence 870, App
38	8	3.3	873	4	US-09-583-110-2322 Sequence 2322, Ap
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41	8	3.3	1587	4	US-09-023-655-1192 Sequence 1192, Ap
42	8	3.3	3207	4	US-09-966-997-10 Sequence 10, Appl
43	8	3.3	5847	4	US-09-962-665-11 Sequence 11, Appl
44	8	3.3	5847	4	US-09-963-333-11 Sequence 11, Appl
45	8	3.3	5847	4	US-09-963-677-11 Sequence 11, Appl

ALIGNMENTS

US-08-869-057-1  
Sequence 1, Application US/08869057  
Patent No. 5985562  
GENERAL INFORMATION:  
APPLICANT: Morset, Michael J  
APPLICANT: Nagashima, Mariko  
TITLE OF INVENTION: Method of Detecting Thrombotic Disease  
TITLE OF INVENTION: Risk  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Berlex Biosciences Legal Department  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,057  
FILING DATE: 03-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L  
REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: 51509AUSM1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1272 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PUBLICATION INFORMATION:
; AUTHORS: Eaton, Dan L.
; AUTHORS: Malloy, Beth E.
; AUTHORS: Tsai, Siao P.
; AUTHORS: Henzel, William
; AUTHORS: Drayna, Dennis
; TITLE: Isolation, Molecular Cloning, and Partial
; TITLE: Characterization of a No. 5985562el Carboxypeptidase B
; TITLE: from Human Plasma
; JOURNAL: J. Biol. Chem.
; VOLUME: 266
; ISSUE: 32
; PAGES: 21833-21838
; DATE: No. 5985562 15-1991
;
US-08-869-057-1
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Pred. No.: 6,4e-148 Length: 1272
Score: 149.00 Matches: 149
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 2 Gaps: 0

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QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
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QY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 1123 GATTGGGCATCAATATTCGTTTACA 1149

RESULT 2
US-07-649-591B-2
; Sequence 2, Application US/07649591B
; Patent No. 5206161
; GENERAL INFORMATION:
; APPLICANT: Dennis Drayna and Daniel Eaton
; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
```

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: hybridization probe
; LOCATION: 133 to 178
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
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; NAME/KEY: potential clip site
; LOCATION: 380 to 382
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
; NAME/KEY: signal sequence
; LOCATION: 41 to 106
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
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US-07-649-591B-2
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Pred. No.: 8,76e-148 Length: 1749
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 1 Gaps: 0

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QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
DB 743 AATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACATCATGTGTCGGAACAGAC 802
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 803 CTGATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGTGCATCCAGTTCCTCATGC 862
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 863 TCGGAACCTACTGTGGACTTATCTCTGAGTCAGAACAGAGTGAAGCGAGTGGTAGT 922
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
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 QY 224 AspLeuGlyIleLysTyrSerPheThr 232  
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RESULT 3  
 US-08-277-540-2  
 ; Sequence 2, Application US/08277540  
 ; Patent No. 5474901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA: 07/959944  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1749 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-277-540-2  
 Alignment Scores:  
 Pred. No.: 8,76e-148 Length: 1749  
 Score: 149.00 Matches: 149  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 60.57% Indels: 0  
 DB: 1 Gaps: 0

US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)  
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 Db 743 AATCGAATGTGGAGAAAGACCGTCTCTTCTATGGAACATCATTCATCGGACAGAC 802  
 QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCys 123  
 Db 803 CTGAATAGGAACTTTGCTTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 862  
 QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValValAlaValAlaSer 143  
 Db 863 TCGGAAACCTACTGTGGACTTTATCTCAGTCAGAACCCAGAGTGAAGCAGTCAGTCTAGT 922  
 QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaIleSerMetHisSerTyrSerGln 163  
 Db 923 TTCCTTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTACTCCCAG 982  
 QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183  
 Db 983 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAGACCATGAGCACTGTCT 1042  
 QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
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 Db 1103 CATGGCCATGGCTCAGAACCTTATACCTCTGGAGGTGGGACGATTGGATCTAT 1162  
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 Db 1163 GATTGGGCATCAATATTCGTTTACA 1189

RESULT 4  
 US-08-430-787A-2  
 ; Sequence 2, Application US/08430787A  
 ; Patent No. 5593674  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/430,787A  
 FILING DATE: 27-APR-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,540  
 FILING DATE: 19-JUL-1994  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA: 07/959944  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1749 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 8.76e-148 Length: 1749  
Score: 149.00 Matches: 149  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 60.57% Indels: 0  
DB: 1 Gaps: 0

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy 84 AsnArgMetTTPATGLyAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGACCGTTCTTCTATATGCGAACAATCATTTGCATCGGAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTGCTTCCAAACACCTGGTGTGAGGAAGGTGCATCCAGTTCTCTCATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 863 TCGGAACCTACTGTGGACTTTATCTCAGTCAGAACACAGAGTGAAGGCCAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCCTTGAGAGGAATATCAACAGATTAAAGCATACATCAGCATGCCATTCATATCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
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Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
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## RESULT 5

US-09-813-133A-1

; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

## Alignment Scores:

Pred. No.: 2.64e-138 Length: 1625  
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Best Local Similarity: 98.29% Mismatches: 2  
Query Match: 56.91% Indels: 4  
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

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Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 419 TTTATAACTGAGAGGCATCCTGATATGCTTTACAAAAATCCACATTTGGATCTCTCATTTGAG 478  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaI 60  
Db 479 AAGTACCCTCTATGTTTTAAAGGTTTCTGGAAAAAGAACAGC-AGCCAAAAAATGCCAT 537  
Qy 60 eTTPileAspCysGlyIleHisAlaArgGluTyrIleSerProAlaPheCysLeuTrpPh 80  
Db 538 ATGGATTGACTGTGGAAATCCATGCCAGAGAAATGGATCTCTCTGCTTTCTGCTTGTGTT 597  
Qy 80 eIleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysI 100  
Db 598 CATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAATCATTTGCAT 657  
Qy 100 eGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSe 120  
Db 658 CGGAACACAGACTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCAG 717  
Qy 120 rSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAl 140  
Db 718 TTCCTCATGTCTCGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACAGAGTGAAGGC 777  
Qy 140 aValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe 160  
Db 778 AGTGGCTAGTTCTTGGAGAAAGAAATATCAACAGATTAAAGCATATACATCAGCATGCTTC 837  
Qy 160 rTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisG 180  
Db 838 ATACTCCAGCATATAGTGTTCCTATATCTATACAGAAAGTAAAGACCAAGACCAATGA 897  
Qy 180 uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnT 200  
Db 898 GGAACCTGCTCTAGTAGCCAGTGNAGCAGTTCGTGCTATTGAGAAAAATT-AGTAAAAATA 956  
Qy 200 hrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAsp 220  
Db 957 CCAGGTATACATGCGCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACG 1016  
Qy 220 sPTTPIleTyrAspLeuGlyIleLysTyrSerPheThr 232  
Db 1017 ATTGGATCTATGATTGGGCATCAAAATATTCTGTTTACA 1054

## RESULT 6

US-09-813-133A-3

; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
;

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; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3
Alignment Scores:
Pred. No.: 1,05e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-3 (1-55827)
Qy 115 GluGluGlyAlaSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 48643 GAGGAAGTGCATCCAGTTCTTCATGCTCGAAACCTACTGTGGACTTTATCCTGAGTCA 48702
Qy 135 GluProGluValIysAlaValAlaSerPheLeuArgAtcAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGAGTCAAGCGATGCTAGTTCTTTGAGAAGAAATATCAACAGATTAAAGCA 48762
Qy 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 174
Db 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATTCCTATACAGAGT 48822
Qy 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 7
US-09-675-305-5
; Sequence 5, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 741
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-5
Alignment Scores:
Pred. No.: 0.0022 Length: 741
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-5 (1-741)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGTATTTCATGCAAGAGATGGATT 603

RESULT 8
US-09-675-305-11
; Sequence 11, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-11
Alignment Scores:
Pred. No.: 0.00311 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-5 (1-741)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGTATTTCATGCAAGAGATGGATT 603

RESULT 8
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US-09-980-881A-4 (1-246) x US-09-675-305-11 (1-1050)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 10
US-10-200-344-11
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-11

Alignment Scores:
Pred. No.: 0.00311 Length: 1050
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-200-344-11 (1-1050)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 11
US-09-675-305-9
; Sequence 9, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0
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Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-9 (1-1311)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 12
US-10-200-344-9
; Sequence 9, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.: 0.00387 Length: 1311
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIle 72
Db 568 TGGATAGACTGTGGTATTTCATGCAAGAGATGGATT 603

RESULT 13
US-09-675-305-13
; Sequence 13, Application US/09675305
; Patent No. 6441153
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/09/675,305
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,685
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-675-305-13

Alignment Scores:
Pred. No.: 0.00625 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-675-305-13 (1-2128)
Qy 61 TptlleAppCysGlyIleHisAlaArgGluTrrPile 72
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGAGATGGATT 968

RESULT 14
US-10-200-344-13
; Sequence 13, Application US/10200344
; Patent No. 6780640
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6780640el Human Carboxypeptidases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-13

Alignment Scores:
Pred. No.: 0.00625 Length: 2128
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.88% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-200-344-13 (1-2128)
Qy 61 TptlleAppCysGlyIleHisAlaArgGluTrrPile 72
Db 933 TGGATAGACTGTGGTATTTCATGCAAGAGAGATGGATT 968
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RESULT 15
US-09-270-767-25119
; Sequence 25119, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25119
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; LENGTH: 258
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25119

Alignment Scores:
Pred. No.: 0.00886 Length: 258
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.47% Indels: 0
DB: 4 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-270-767-25119 (1-258)
Qy 65 GlyIleHisAlaArgGluTrrPileSerProAla 75
Db 127 GGCATCCACGCCCGGGAATGGATCAGCCCCGCG 159

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1  
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Database : Published Applications NA:

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- 2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:
- 3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:
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- 5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq:
- 6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq:
- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:
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- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:
- 15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:
- 16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:
- 17: /cgn2\_6/prodata/2/pubpna/US10E\_PUBCOMB.seq:
- 18: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:
- 19: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq:
- 20: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:
- 21: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	149	60.6	1400	9	US-09-925-302-24	Sequence 24, Appl
2	149	60.6	1400	10	US-09-925-302-24	Sequence 24, Appl
3	149	60.6	1728	9	US-09-880-107-2396	Sequence 2396, Ap
4	140	56.9	1625	9	US-09-813-133A-1	Sequence 1, Appli
5	140	56.9	1625	14	US-10-212-877-1	Sequence 1, Appli
6	112	45.5	1344	16	US-10-115-479-69	Sequence 69, Appl
7	112	45.5	1743	16	US-10-115-479-67	Sequence 67, Appl
8	68	27.6	1037	16	US-10-115-479-63	Sequence 63, Appl
9	68	27.6	55827	9	US-09-813-133A-3	Sequence 3, Appli
10	68	27.6	55827	14	US-10-212-877-3	Sequence 65, Appl
11	52	21.1	1132	16	US-10-115-479-65	Sequence 265133,
12	43	17.5	1547	13	US-10-027-632-265133	Sequence 265134,
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15	43	17.5	1547	13	US-10-027-632-265136	Sequence 265137,
16	43	17.5	1547	15	US-10-027-632-265133	Sequence 265134,
17	43	17.5	1547	15	US-10-027-632-265134	Sequence 265135,
18	43	17.5	1547	15	US-10-027-632-265135	Sequence 265136,
19	43	17.5	1547	15	US-10-027-632-265136	Sequence 1, Appli
20	42	17.1	1272	15	US-10-379-836-1	Sequence 14555, A
21	17	6.9	416	9	US-09-960-332-14595	Sequence 26009, A
22	16	6.5	65	10	US-09-908-975-26009	Sequence 468, App
23	14	5.7	431	9	US-09-917-800A-468	Sequence 25938, A
24	13	5.3	65	10	US-09-908-975-25938	Sequence 5, Appli
25	12	4.9	741	13	US-10-200-344-5	Sequence 1, Appli
26	12	4.9	948	9	US-09-888-615-1	Sequence 11, Appl
27	12	4.9	1050	13	US-10-200-344-11	Sequence 13457, A
28	12	4.9	1187	14	US-10-198-846-13457	Sequence 148, App
29	12	4.9	1295	17	US-10-363-829-148	Sequence 1, Appli
30	12	4.9	1302	17	US-10-477-515-1	Sequence 9, Appli
31	12	4.9	1311	13	US-10-200-344-9	Sequence 127, App
32	12	4.9	1907	18	US-10-757-262-127	Sequence 33, Appl
33	12	4.9	1993	15	US-10-274-639-33	Sequence 13, Appl
34	12	4.9	1993	16	US-10-333-574-33	Sequence 3042, Ap
35	12	4.5	2128	13	US-10-200-344-13	Sequence 3068, Ap
36	11	4.5	230	14	US-10-060-036-3042	Sequence 3096, Ap
37	11	4.5	230	14	US-10-060-036-3068	Sequence 3131, Ap
38	11	4.5	230	14	US-10-060-036-3096	Sequence 3150, Ap
39	11	4.5	230	14	US-10-060-036-3131	Sequence 3153, Ap
40	11	4.5	230	14	US-10-060-036-3150	Sequence 3164, Ap
41	11	4.5	230	14	US-10-060-036-3153	Sequence 3175, Ap
42	11	4.5	230	14	US-10-060-036-3164	Sequence 3181, Ap
43	11	4.5	230	14	US-10-060-036-3168	
44	11	4.5	230	14	US-10-060-036-3175	
45	11	4.5	230	14	US-10-060-036-3181	

ALIGNMENTS

RESULT 1  
US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 2,22e-146 Length: 1400
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 179 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTCGATCGGAACAGAC 238
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 239 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 298
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 299 TCGGAACCTACTGTGGACCTTTATCCTGAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 358
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 359 TTCCTTGAGAGAAATATCAACAGATTAAAGCAGATACATCAGCATGCATTCATCTCCAG 418
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 419 CATATAGTGTTCATATATTCCTATACAGAAAGTAAAGCAAGCAACCATGAGGAACCTGTCT 478
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 479 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 538
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223
DB 539 CATGCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGGTGGGACGATTGGATCTAT 598

RESULT 2
US-09-925-302-24
; Sequence 24, Application US/0925302
; Publication NO. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-24

Alignment Scores:
Pred. No.: 2,22e-146 Length: 1400
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 179 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACATCATTCGATCGGAACAGAC 238
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 239 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 298
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 299 TCGGAACCTACTGTGGACCTTTATCCTGAGTCAGAACAGAGTGAAGCGAGTGGCTAGT 358
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 359 TTCCTTGAGAGAAATATCAACAGATTAAAGCAGATACATCAGCATGCATTCATCTCCAG 418
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 419 CATATAGTGTTCATATATTCCTATACAGAAAGTAAAGCAAGCAACCATGAGGAACCTGTCT 478
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 479 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 538
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223
DB 539 CATGCCATGGCTCAGAAACCTTATACCTAGCTCTGGAGGTGGGACGATTGGATCTAT 598

RESULT 3
US-09-880-107-2396
; Sequence 2396, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2396
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106
US-09-880-107-2396

Alignment Scores:
Pred. No.: 2,71e-146 Length: 1728
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0

```

Best Local Similarity: 100.00%				Mismatches: 0
Query Match: 60.57%				Indels: 0
DB:				Gaps: 0
US-09-980-881A-4 (1-246) x US-09-880-107-2396 (1-1728)				
QY	84	AsnArgMetTrrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysileGlyThrAsp	103	
DB	722	ATCGATGTCGGAGAAAGACCGTTCTTCTATGCGAACAAATCATTTGCATCGGAACAGAC	781	
QY	104	LeuAsnArgAsnPheAlaSerLysHisTrrCysGluGluGlyAlaSerSerSerCys	123	
DB	782	CTGAATAGGAACCTTTCCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC	841	
QY	124	SerGluThrTyrCysGlyLeuTrrProGluSerGluProGluValLysAlaValAlaSer	143	
DB	842	TCGGAACCTTACTGTGGACTTATCTCTGAGTCAGAACCAAGTAGGAGCAGTGGCTAGT	901	
QY	144	PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln	163	
DB	902	TTCCTTGAGAAAGAAATATCAACGATTAAGCATACATCAGCATGCAATTCATACCCCAG	961	
QY	164	HisIleValPheProTrrSerTrrTrrArgSerLysSerLysAspHisGluLeuSer	183	
DB	962	CATATAGTGTTCCTATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACGTCT	1021	
QY	184	LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTrrThr	203	
DB	1022	CTAGTAGCCAGTGAACGAGTTCGTGTATTTGAGAAACCTAGTAAATAATACCGAGTATACA	1081	
QY	204	HisGlyHisGlySerGluThrLeuTrrLeuAlaProGlyGlyGlyAspTrrPileTyr	223	
DB	1082	CATGGCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGTGGGACGATGGATCTAT	1141	
QY	224	AppLeuGlyLysTrrSerPheThr	232	
DB	1142	GATTTGGCATCAATATTCGTTTACA	1168	
RESULT 4				
US-09-813-133A-1				
; Sequence 1, Application US/09813133A				
; Publication No. US20020137179A1				
; GENERAL INFORMATION:				
; APPLICANT: GAN, Weiniu et al				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; TITLE OF INVENTION: USES THEREOF				
; FILE REFERENCE: CL001173				
; CURRENT APPLICATION NUMBER: US/09/813,133A				
; CURRENT FILING DATE: 2001-06-06				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 1				
; LENGTH: 1625				
; TYPE: DNA				
; ORGANISM: Human				
US-09-813-133A-1				
Alignment Scores:				
Pred. No.:	7,24e-137	Length:	1625	
Score:	140.00	Matches:	230	
Percent Similarity:	98.29%	Conservative:	0	
Best Local Similarity:	98.29%	Mismatches:	2	
Query Match:	56.91%	Indels:	4	
DB:	9	Gaps:	0	
US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)				
QY	1	AlaSerAlaSerTrrTrrGluThrHisSerLeuAsnGluLysTrrSerTrrPileGlu	20	
DB	359	GCCTCCGCATCGTACTATGAACAGTATCACTCAATAATGAAATCTATTCCTGGATAGAA	418	
QY	21	PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu	40	

DB	419	TTTATAACTGAGAGGCATCCTGATGCTTACAAAAATCCCATTTGGATCCTCATTTGAG	478	
QY	41	LysTrrProLeuTrrValLeuLysValSerGlyLysGluGlnThr-AlaLysAsnAlaIle	60	
DB	479	AAGTACCACCTCTATGTTTTTAAGGTTCTCGAAAAAGAACAGC-AGCCAAAAATGCCAT	537	
QY	60	eTrrPileAspCysGlyIleHisAlaArgGluTrrPileSerProAlaPheCysLeuTrrPhe	80	
DB	538	ATGGATTGACTGTGGAATCCATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTGTGGTT	597	
QY	80	eIleGlyHisAsnArgMetTrrArgLysAsnArgSerPheTrrAlaAsnAsnHisCysIle	100	
DB	598	CATAGGCCATATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAACAAATCATTTGCAT	657	
QY	100	eGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrrCysGluGluGlyValaSerSe	120	
DB	658	CGGAACACACCTGAATAGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAG	717	
QY	120	rSerSerCysSerGluThrTrrCysGlyLeuTrrProGluSerGluProGluValLysAl	140	
DB	718	TTCTCTCATGCTCGGAACCTACTGTGGACTTTATCTGAGTCAGAACCAAGAGTGAAGGC	777	
QY	140	aValAlaSerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe	160	
DB	778	AGTGCTAGTTTCTTGAGAGAAATATCAACACAGATTAAAGCATACATCAGCATGCATTC	837	
QY	160	rTrrSerGlnHisIleValPheProTrrSerTrrTrrArgSerLysSerLysAspHisG1	180	
DB	838	ATATCTCCAGCATATAGTGTTTCCATATTCCTATACAGAAAGTAAAGCAAGACCATGA	897	
QY	180	uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnT	200	
DB	898	GGAACTGCTCTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAAATT-AGTAAAAATA	956	
QY	200	hrArgTrrThrHisGlyHisGlySerGluThrLeuTrrLeuAlaProGlyGlyGlyAspA	220	
DB	957	CCAGGTATACATCATGCGCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGTGGGACG	1016	
QY	220	spTrrPileTrrAspLeuGlyIleLysTrrSerPheThr	232	
DB	1017	ATTGGATCTATGATTGGGCATCAAAATATTCGTTTACA	1054	
RESULT 5				
US-10-212-877-1				
; Sequence 1, Application US/10212877				
; Publication No. US200300017574A1				
; GENERAL INFORMATION:				
; APPLICANT: GAN, Weiniu et al				
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,				
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND				
; TITLE OF INVENTION: USES THEREOF				
; FILE REFERENCE: CL001173DIV				
; CURRENT APPLICATION NUMBER: US/10/212,877				
; CURRENT FILING DATE: 2002-08-07				
; PRIOR APPLICATION NUMBER: 09/813,133				
; PRIOR FILING DATE: 2001-03-21				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 1				
; LENGTH: 1625				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-10-212-877-1				
Alignment Scores:				
Pred. No.:	7,24e-137	Length:	1625	
Score:	140.00	Matches:	230	
Percent Similarity:	98.29%	Conservative:	0	
Best Local Similarity:	98.29%	Mismatches:	2	
Query Match:	56.91%	Indels:	4	
DB:	14	Gaps:	0	

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US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGATACCTCACTCACTAAATGAAATCTATTCTTGGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGGCATCCTGATATGCTTCAAAAAATCCCATTTGGATCCTCATTTTGGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCACCTCTATGTTTAAAGTTTCTTGAAAAGAACAGC-AGCCAAAAATGCCAT 537
Qy 60 eTrpIleAspCysGlyIleHisAlaArgLutrpIleSerProAlaPheCysLeuTrpPh 80
Db 538 ATGGATTGACGTGGAATCCATGCCAGAGAATGGATCTCTCTGCTTCTGCTTGTGTT 597
Qy 80 eIleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 598 CATAGGCCATAATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCAT 657
Qy 100 eGlyThrAspLeuAsnArgAsnPheAlaSerIleHisTrpCysGluGluGlyAlaSerSe 120
Db 658 CGGAACAGACCTGGAATAGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAG 717
Qy 120 rSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAl 140
Db 718 TTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGGC 777
Qy 140 aValAlaSerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSe 160
Db 778 AGTGCTAGTTCTTTGAGAAGAAATATCAACCAGATTAAAGCATATACATCAGCATGCATTC 837
Qy 160 rTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGl 180
Db 838 ATACTCCAGCATATAGTGTTCATATTCCATATACAGAAATGTAAGAAAGAACCATGA 897
Qy 180 uGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnT 200
Db 898 GGAAGTGTCTCTAGTAGCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAAAATA 956
Qy 200 hrArgTyrThrHisGlyHisGlySerGluThrLeuTyrIleuAlaProGlyGlyAspA 220
Db 957 CCAGGTATACACATGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGAGGTGGGACG 1016
Qy 220 spTrpIleTyrAspLeuGlyIleLysTyrSerPheThr 232
Db 1017 ATTGGATCATATGTTGGGCATCAAAATATTGTTTACA 1054

RESULT 6
US-10-115-479-69
; Sequence 69, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei

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; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,697
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.: 1.54e-107 Length: 1344
Score: 112.00 Matches: 148
Percent Similarity: 98.67% Conservative: 0
Best Local Similarity: 98.67% Mismatches: 1
Query Match: 45.53% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 748 AATCGAATGTGGAGAAAGAACCCGTTCTTTCTATCGGAACAATCATTCATCGGAACAGAC 807
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 808 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 867
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 868 TCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACAGAACGAGGCGAGTGGCTAGT 927
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 928 TTCCTGAGAGAAATATCAACAGATTAAAGCATACATCAGCATTCATCTATCTCCAG 987
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 988 CATATAGTGTTCCTATATTCCTATACAGGAAGTAAAGCAAGACCATGAGGAAGTGTCT 1047

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QY 184 LeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrTh 203
Db 1048 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAATAACAGGTATAC 1106
QY 203 rHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTy 223
Db 1107 ACATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTA 1166
QY 223 rAspLeuGlyIleLysTyrSerPheThr 232
Db 1167 TGATTGGGCATCAAAATATTGTTTACA 1194

RESULT 7
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication NO. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Fatturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20) .. (1304)
US-10-115-479-67
Alignment Scores:
Pred. No.: 1,97e-107 Length: 1743
Score: 112.00 Matches: 148
Percent Similarity: 98.67% Conservative: 0
Best local Similarity: 98.67% Mismatches: 1
Query Match: 45.53% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)
QY 84 AsnArgMetTyrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 737 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGCGAAACAATCATTTGCATCGGAACAGAC 796
QY 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123
Db 797 CTGAATAGAACTTTGCTTCCAAACACCTGGTGTGAGGAAGTGCATCCAGTTCCTCATGC 856
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db 857 TCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGTGAAGCAGTGGCTAGT 916
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db 917 TTCTTGAGAAGAAATATCAACCAAGATTAAAGCATACATCAGCATCATCTACTCTCCAG 976
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 977 CATATAGTGTTCATATTCCTATACAGAGTAAAGCAAAAGCAACCATGAGGAACCTGTCT 1036
QY 184 LeuValAlaSerGluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrTh 203
Db 1037 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAT-AGTAAATAACAGGTATAC 1095
QY 203 rHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTy 223
Db 1096 ACATGCCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTA 1155

RESULT 8
US-10-115-479-63
; Sequence 63, Application US/10115479
; Publication NO. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
```

```
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 1,96e-61 Length: 1037
Score: 68.00 Matches: 104
Percent Similarity: 98.11% Conservative: 0
Best Local Similarity: 98.11% Mismatches: 1
Query Match: 27.64% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)

Qy 128 CysGlyLeuTyrProGluSerGluProGluVallylsAlaValAlaSerPheLeuArg 147
Db 572 TGTGGACTTATCTCTGAGTCAGAACAGAGAGTGAAGCGAGTGGCTTCTTCTGAGAAGA 631
Qy 148 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 167
Db 632 AATATCAACCAAGATTAAAGCATATCATGATGCATCTTCTACTCCAGCATATAGTGT 691
Qy 168 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSer 187
Db 692 CCATATTCTTATACAGGAAGTAAAGCAAGACCATGAGGAACGTCTCTAGTAGCCAGT 751
Qy 188 GluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrThrHisGlyHisG1 207
Db 752 GAAGCAGTTCGTGCTATTGAGAAAAATT-AGTAAAAATACCAAGGTATACACATGGCCATGG 810
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyI1 227
Db 811 CTCGAAACCTTATACCTAGTCTCTGGAGTGGGAGCAACGATTGGATCTATGATTGGGCAT 870

; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 63
; LENGTH: 1037.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)...(1007)
US-10-115-479-63

Alignment Scores:
Pred. No.: 1,96e-61 Length: 1037
Score: 68.00 Matches: 104
Percent Similarity: 98.11% Conservative: 0
Best Local Similarity: 98.11% Mismatches: 1
Query Match: 27.64% Indels: 2
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)

Qy 128 CysGlyLeuTyrProGluSerGluProGluVallylsAlaValAlaSerPheLeuArg 147
Db 572 TGTGGACTTATCTCTGAGTCAGAACAGAGAGTGAAGCGAGTGGCTTCTTCTGAGAAGA 631
Qy 148 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 167
Db 632 AATATCAACCAAGATTAAAGCATATCATGATGCATCTTCTACTCCAGCATATAGTGT 691
Qy 168 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSer 187
Db 692 CCATATTCTTATACAGGAAGTAAAGCAAGACCATGAGGAACGTCTCTAGTAGCCAGT 751
Qy 188 GluAlaValArgAlaIleGlu-LysThrSerLysAsnThrArgTyrThrHisGlyHisG1 207
Db 752 GAAGCAGTTCGTGCTATTGAGAAAAATT-AGTAAAAATACCAAGGTATACACATGGCCATGG 810
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyI1 227
Db 811 CTCGAAACCTTATACCTAGTCTCTGGAGTGGGAGCAACGATTGGATCTATGATTGGGCAT 870
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Qy 227 eLysTyrSerPheThr 232
Db 871 CAAATATTCGTTTACA 886

RESULT 9
US-09-813-133A-3
; Sequence 3, Application US/09813133A
; Publication No. US20020137179A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinui et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-3

Alignment Scores:
Pred. No.: 8.46e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 9 Gaps: 0

US-09-980-881A-4 (1-246) x US-09-813-133A-3 (1-55827)

Qy 115 GluGluGlyAlaSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 48643 GAGGAAGTGCATCCAGTTCCTCATGCTCGGAACCTACTGTGGACTTTATCTCTGAGTCA 48702
Qy 135 GluProGluVallylsAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 48762
Qy 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 174
Db 48763 TACATCAGCATGCATTCATCTCCAGCATATAGTGTTCATATCTCTATACACGAAGT 48822
Qy 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAACGTG 48846

RESULT 10
US-10-212-877-3
; Sequence 3, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinui et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 55827
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-3

Alignment Scores:
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Pred. No.: 8,46e-60 Length: 55827
Score: 68.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.64% Indels: 0
DB: 14 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-212-877-3 (1-55827)

QY 115 GluGluGlyAlaSerSerSerSerGluThrTyrCysGlyLeuTyrProGluSer 134
Db 48643 GAGGAAGTGCATCCAGTTCCTCATGCTCGAAACCTACTGTGGACTTTATCTCGAGTCA 48702

QY 135 GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
Db 48703 GAACCAAGAGTGAAGCAGTGGCTAGTTCTTGAGAAGAAATATCAACCAAGATTAAAGCA 48762

QY 155 TyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSer 174
Db 48763 TACATCAGATGCATTCATCTCCAGCATATAGTGTTCCTATATTCCTATACGAAAGT 48822

QY 175 LysSerLysAspHisGluGluLeu 182
Db 48823 AAAAGCAAGACCATGAGGAAGT 48846

RESULT 11
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spyttek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Hailong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
US-10-115-479-65

Alignment Scores:
Pred. No.: 1,35e-44 Length: 1132
Score: 52.00 Matches: 52
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.14% Indels: 0
DB: 16 Gaps: 0

US-09-980-881A-4 (1-246) x US-10-115-479-65 (1-1132)

QY 84 AsnArgMetTyrArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 758 AATCGAATGTGGAGAAAGACCGTTCTTTCTATGCGAAACAATCATTCATCGGAACAGAC 817

QY 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaSerSerSerCys 123
Db 818 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAGGTGCATCCAGTTCCTCATGC 877

QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGlu 135
Db 878 TCGGAACCTACTGTGGACTTTATCTCGATCAGAA 913

RESULT 12
US-10-027-632-265133
; Sequence 265133, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265133
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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[illegible]



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US-10-027-632-265136
; Sequence 265136, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 265136
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1547)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-265136

Alignment Scores:
Pred. No.:      5,14e-35      Length:      1547
Score:          43.00        Matches:     43
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:      17.48%     Indels:      0
DB:              13         Gaps:       0

US-09-980-881A-4 (1-246) x US-10-027-632-265136 (1-1547)

Qy      115  GluGluGlyAlaSerSerSerCysSerCluThrTyrCysGlyLeuTyProGluSer 134
      |||
Db      1417  GAGGAAGGTGCATCCCAATTCTCATGCTCGGAACCTACTGTGGACTTTATCTCGTGTC 1476

Qy      135  GluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAla 154
      |||
Db      1477  GAACCAGAAGTGAAGCGATGGTAGTTCTTGTGAGAGAANAATCAACCAGATTAAAGCA 1536

Qy      155  TyrIleSer 157
      |||||
Db      1537  TACATCAGC 1545

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Search completed: October 27, 2004, 09:21:50  
Job time : 367.475 secs





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Db      2 HHC-----YRKKFHEKHHCHRG 18

RESULT 5
US-09-693-822B-23
; Sequence 23, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-23

Query Match      3.0%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1e+03;
Matches      8; Conservative      1; Mismatches      8; Indels      4; Gaps      1;

QY      97 NHCIGTDLNRNFASKHWCBEQ 117
;
;
;
Db      2 HHC-----YRKKFHEKHHCHRG 18

RESULT 6
US-09-693-822B-24
; Sequence 24, Application US/09693822B
; Patent No. 6555650
; GENERAL INFORMATION:
; APPLICANT: Lajoie, Gilles A.
; TITLE OF INVENTION: Cyclic Analogs of Histatins
; FILE REFERENCE: 36555-0002
; CURRENT APPLICATION NUMBER: US/09/693,822B
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: CA 2,285,673
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cyclic analogues of histatin
US-09-693-822B-24

Query Match      3.0%; Score 40; DB 4; Length 19;
Best Local Similarity 38.1%; Pred. No. 1e+03;
Matches      8; Conservative      1; Mismatches      8; Indels      4; Gaps      1;

QY      97 NHCIGTDLNRNFASKHWCBEQ 117
;
;
;
Db      2 HHC-----YRKKFHEKHHCHRG 18

RESULT 7
US-09-402-641-1
; Sequence 1, Application US/09402641
; Patent No. 6528619
; GENERAL INFORMATION:
; APPLICANT: BUERGLE, Markus
; APPLICANT: GRAEFF, Heinrich

```

;; APPLICANT: KESSLER, Horst  
;; APPLICANT: MAGDOLEN, Viktor Robert  
;; APPLICANT: KOENIG, Bernhard  
;; APPLICANT: KOPPIZ, Marcus  
;; APPLICANT: RIEMER, Christoph  
;; APPLICANT: SCHMITT, Manfred  
;; APPLICANT: WEIDLE, Ulrich  
;; APPLICANT: WILHELM, Olaf  
;; TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR  
;; FILE REFERENCE: Case 2036705  
;; CURRENT APPLICATION NUMBER: US/09/402,641  
;; CURRENT FILING DATE: 2000-01-10  
;; PRIOR APPLICATION NUMBER: EP97106024.9  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: PCT/EP98/02178  
;; PRIOR FILING DATE: 1998-04-14  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 13  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide "cyclo  
;; OTHER INFORMATION: 19.31 UPA 19-31"; Figure 3A  
US-09-402-641-1  
  
Query Match 3.0%; Score 39.5; DB 4; Length 13;  
Best Local Similarity 37.5%; Pred. No. 6.5e+02;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;  
  
QY 99 CIGTDLNRNFASKHWC 114  
Db 1 CVS---NKYFSNIHWC 13  
  
RESULT 8  
US-08-142-590B-5  
; Sequence 5, Application US/08142590B  
; Patent No. 6120765  
; GENERAL INFORMATION:  
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and  
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,590B  
; FILING DATE: 25-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,318  
; FILING DATE: 02-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REFERENCE/DOCKET NUMBER: 35,965  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid

;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-142-590B-5  
  
Query Match 3.0%; Score 39.5; DB 3; Length 15;  
Best Local Similarity 37.5%; Pred. No. 8.1e+02;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;  
  
QY 99 CIGTDLNRNFASKHWC 114  
Db 2 CVS---NKYFSNIHWC 14  
  
RESULT 9  
US-08-747-915-4  
; Sequence 4, Application US/08747915  
; Patent No. 5942492  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Terence R.  
; APPLICANT: Haney, David N.  
; APPLICANT: Varga, Janos  
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO  
; TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,915  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 32904-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEFAX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-747-915-4  
  
Query Match 3.0%; Score 39.5; DB 2; Length 18;  
Best Local Similarity 37.5%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;  
  
QY 99 CIGTDLNRNFASKHWC 114  
Db 3 CVS---NKYFSNIHWC 15  
  
RESULT 10  
US-08-467-023-211  
; Sequence 211, Application US/08467023  
; Patent No. 6090386  
; GENERAL INFORMATION:  
; APPLICANT: Griffeth, Irwin J.;  
; APPLICANT: Pollock, Joanne;

```

; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,023
; FILING DATE: June 6, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,225
; FILING DATE: December 6, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-467-023-211

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Query Match 3.0%; Score 39.5; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Qy 52 KEQTANQNAIWD 63
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Db 2 KERTATN-IWID 12

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RESULT 11
US-08-142-590B-4
; Sequence 4, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-142-590B-4

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Query Match 3.0%; Score 39.5; DB 3; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

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Qy 99 CIGTDLNRNFASKHWC 114
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Db 5 CVS---NKYFSNIHWC 17

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RESULT 12
US-08-142-590B-24
; Sequence 24, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-142-590B-24

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Search completed: October 27, 2004, 01:31:43  
Job time : 12.7691 secs







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RESULT 2
US-10-343-509-10
; Sequence 10, Application US/10343509
; Publication No. US20040101865A1
; GENERAL INFORMATION:
; APPLICANT: BASF
; TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
; FILE REFERENCE: 0050/51654
; CURRENT APPLICATION NUMBER: US/10/343,509
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRP
; ORGANISM: Euglena gracilis
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = (Phe/Tyr)
US-10-343-509-10

Query Match 3.6%; Score 48; DB 16; Length 11;
Best Local Similarity 70.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 217 GGDHWYDLG 226
||| |||:|
Db 1 GGDGWYDIG 10

RESULT 3
US-10-410-764-87
; Sequence 87, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; FILE REFERENCE: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520NNIM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 11
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Zinc carboxypeptidase zinc-binding region 2
US-10-410-764-87

Query Match 3.4%; Score 46; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 5.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 159 HSYSQHIVFPY 169
||||| :|||
Db 1 HSYSQLMYPY 11

RESULT 4
US-09-825-517A-44
; Sequence 44, Application US/09825517A
; Publication No. US20030203415A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
; FILE REFERENCE: DYX-016.1 (3421, 1005-001)
; CURRENT APPLICATION NUMBER: US/09/825,517A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/541,345
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-44

Query Match 3.2%; Score 42.5; DB 10; Length 16;
Best Local Similarity 43.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 60 IWDCGIHAREWISPA 75
||| |||:|
Db 1 IW-DCNLFKNQWFCPA 15

RESULT 5
US-10-742-379-90
; Sequence 90, Application US/10742379
; Publication No. US20040181033A1
; GENERAL INFORMATION:
; APPLICANT: Han, HQ
; APPLICANT: Min, Hosung
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REFERENCE: A-828 (US)
; CURRENT APPLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,923
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 18
; TYPE: PRP
; ORGANISM: Artificial Sequence
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RESULT 9
US-09-791-524-1
; Sequence 1, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Adenovirus
; US-09-791-524-1

Query Match          3.0%; Score 39.5; DB 10; Length 19;
Best Local Similarity 37.5%; Pred. No. 5.8e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy 99 CIGTDLNRFASKHWC 114
| : | : | : |
Db 6 CVS---NKYFSNIHWC 18

RESULT 10
US-09-791-524-2
; Sequence 2, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Adenovirus
; US-09-791-524-2

Query Match          2.9%; Score 39; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 105 NNFASKHWC 114
| : | : |
Db 9 NKYFSNIHWC 18

RESULT 11
US-09-822-624-20
; Sequence 20, Application US/09822624
; Publication No. US2002004233A1
; GENERAL INFORMATION:
; APPLICANT: Abell, Creed W.
; APPLICANT: Kwan, Sua-Wah
; APPLICANT: Zhou, Binnua
; APPLICANT: Wo, Bo
; TITLE OF INVENTION: Tyr393 and Tyr398 Mutants of Monoamine Oxidase B
; FILE REFERENCE: D6237PCT
; CURRENT APPLICATION NUMBER: US/09/822,624
; CURRENT FILING DATE: 2001-03-30
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; PRIOR APPLICATION NUMBER: 2000-03-30
; PRIOR FILING DATE: US 60/193,178
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence flanking the covalent FAD
; OTHER INFORMATION: binding residue of human monooxidase B (MAO B)
US-09-822-624-20

Query Match          2.9%; Score 38.5; DB 9; Length 17;
Best Local Similarity 53.3%; Pred. No. 6.4e+03;
Matches 8; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 113 WCEGASSSCSETY 127
| | | | |
Db 1 WCEB-QYSGGYTTY 14

RESULT 12
US-09-728-721-47
; Sequence 47, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-728-721-47

Query Match          2.8%; Score 38; DB 9; Length 16;
Best Local Similarity 52.6%; Pred. No. 6.6e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

Qy 127 YCGLYPESEPEVKAVASFL 145
| | | | |
Db 1 YC--YPERDPE--EVFAFL 15

RESULT 13
US-10-295-981-47
; Sequence 47, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
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; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 47  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-295-981-47

Query Match 2.8%; Score 38; DB 14; Length 16;  
 Best Local Similarity 52.6%; Pred. No. 6.6e+03;  
 Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 2;

QY 127 YCGLYPESEPEVKAVASFL 145  
 || ||| :|| :||  
 Db 1 YC--YPERDPE--EVFAFL 15

RESULT 14  
 US-10-125-869A-23  
 ; Sequence 23, Application US/10125869A  
 ; Publication No. US20030199671A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rondon, Isaac Jesus  
 ; APPLICANT: Wu, Qi-Long  
 ; APPLICANT: Ley, Arthur C.  
 ; APPLICANT: Stochl, Mark  
 ; APPLICANT: Ranschoff, Thomas C.  
 ; APPLICANT: Potter, M. Daniel (deceased)  
 ; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION  
 ; TITLE OF INVENTION: POLYPEPTIDES  
 ; FILE REFERENCE: 3421.1006-001  
 ; CURRENT APPLICATION NUMBER: US/10/125,869A  
 ; CURRENT FILING DATE: 2002-11-19  
 ; PRIOR APPLICATION NUMBER: 60/284,534  
 ; PRIOR FILING DATE: 2001-04-18  
 ; NUMBER OF SEQ ID NOS: 200  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fc region binding polypeptide  
 US-10-125-869A-23

Query Match 2.8%; Score 38; DB 14; Length 18;  
 Best Local Similarity 35.0%; Pred. No. 7.8e+03;  
 Matches 7; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 64 CGIHAREWISPAFCLWFIGH 83  
 | :| :| :| :|  
 Db 1 CRACSRDW--PGALVWCAGH 18

RESULT 15  
 US-10-462-262-247  
 ; Sequence 247, Application US/10462262  
 ; Publication No. US20040009534A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sato, Aaron K.  
 ; APPLICANT: Dawson, Bruce M.  
 ; TITLE OF INVENTION: PROTEIN ANALYSIS  
 ; FILE REFERENCE: 10280-052001  
 ; CURRENT APPLICATION NUMBER: US/10/462,262  
 ; CURRENT FILING DATE: 2003-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/388,642  
 ; PRIOR FILING DATE: 2002-06-14  
 ; NUMBER OF SEQ ID NOS: 430  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 247

; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: immunoglobulin binding polypeptide  
 US-10-462-262-247

Query Match 2.8%; Score 38; DB 15; Length 18;  
 Best Local Similarity 35.0%; Pred. No. 7.8e+03;  
 Matches 7; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 64 CGIHAREWISPAFCLWFIGH 83  
 | :| :| :| :|  
 Db 1 CRACSRDW--PGALVWCAGH 18

Search completed: October 27, 2004, 01:43:17  
 Job time : 32.0106 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:43:22 ; Search time 64.6271 Seconds  
(without alignments)  
2705.583 Million cell updates/sec

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Perfect score: 1338  
Sequence: 1 ASASYEQHSINETYWIE.....IKYFSTSPNPVKKLLPLSLK 246

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-O=/cgn2\_1/USPTO spooll\_p/US0980881/runat 26102004 084114 7227/app query.fasta\_1.1429  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=std.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*				4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*							
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1	1289.5	96.4	1625	4	US-09-813-133A-1	Sequence 1, Appli					
2	1272	95.1	1272	2	US-08-869-057-1	Sequence 1, Appli					
3	1272	95.1	1749	1	US-07-649-591B-2	Sequence 2, Appli					
4	1272	95.1	1749	1	US-08-277-540-2	Sequence 2, Appli					
5	1272	95.1	1749	1	US-08-430-787A-2	Sequence 2, Appli					
6	610	45.6	927	2	US-08-782-760-5	Sequence 5, Appli					
7	610	45.6	927	5	PCT-US96-00995-5	Sequence 5, Appli					
8	582	43.5	921	1	US-08-696-139-3	Sequence 3, Appli					
9	582	43.5	1215	1	US-08-696-139-1	Sequence 1, Appli					
10	567	42.4	999	2	US-08-860-882A-67	Sequence 67, Appl					
11	567	42.4	999	4	US-09-011-769A-50	Sequence 50, Appl					
12	567	42.4	1053	2	US-08-860-882A-64	Sequence 64, Appl					

13	567	42.4	1053	4	US-09-011-769A-46	Sequence 46, Appli
14	567	42.4	1263	2	US-08-860-882A-56	Sequence 56, Appli
15	567	42.4	1263	4	US-09-011-769A-38	Sequence 38, Appli
16	567	42.4	1284	2	US-08-860-882A-71	Sequence 71, Appli
17	567	42.4	1284	4	US-09-011-769A-55	Sequence 55, Appli
18	567	42.4	1053	4	US-09-463-451-27	Sequence 27, Appli
19	560	41.9	1053	4	US-09-463-451-28	Sequence 28, Appli
20	560	41.9	1059	2	US-08-860-882A-74	Sequence 74, Appli
21	560	41.9	1059	2	US-09-011-769A-59	Sequence 59, Appli
22	559	41.8	1059	2	US-08-860-882A-77	Sequence 77, Appli
23	559	41.8	1059	4	US-09-011-769A-63	Sequence 63, Appli
24	556.5	41.6	1311	4	US-09-675-305-9	Sequence 9, Appli
25	556.5	41.6	1311	4	US-10-200-344-9	Sequence 9, Appli
26	552	41.3	1622	4	US-09-023-655-1020	Sequence 1020, Ap
27	549	41.0	1870	3	US-09-171-945-112	Sequence 112, App
28	549	41.0	2154	3	US-09-171-945-124	Sequence 124, App
29	525.5	39.3	2128	4	US-09-675-305-13	Sequence 13, Appli
30	525.5	39.3	2128	4	US-10-200-344-13	Sequence 13, Appli
31	492	36.8	1200	4	US-09-710-099-7	Sequence 7, Appli
32	492	36.8	1200	4	US-10-200-910-7	Sequence 7, Appli
33	471.5	35.2	1050	4	US-09-675-305-11	Sequence 11, Appli
34	471.5	35.2	1050	4	US-10-200-344-11	Sequence 11, Appli
35	465.5	34.8	1257	3	US-08-640-906-1	Sequence 1, Appli
36	465.5	34.8	1257	3	US-09-395-936-1	Sequence 5, Appli
37	465.5	34.8	1311	4	US-09-710-099-5	Sequence 5, Appli
38	465.5	34.8	1311	4	US-10-200-910-5	Sequence 3, Appli
39	459	34.3	1251	3	US-08-640-906-3	Sequence 3, Appli
40	459	34.3	1251	3	US-09-395-936-3	Sequence 3, Appli
41	405.5	30.3	945	4	US-09-710-099-3	Sequence 11, Appli
42	405.5	30.3	945	4	US-09-710-099-11	Sequence 3, Appli
43	405.5	30.3	945	4	US-10-200-910-3	Sequence 11, Appli
44	405.5	30.3	945	4	US-10-200-910-11	Sequence 11, Appli
45	403.5	30.2	2247	4	US-09-710-099-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CLO01173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1  
Alignment Scores:  
Pred. No.: 3.46e-156 Length: 1625  
Score: 1289.50 Matches: 244  
Percent Similarity: 92.42% Conservative: 0  
Best Local Similarity: 92.42% Mismatches: 2  
Query Match: 96.38% Indels: 18  
DB: 4 Gaps: 1  
US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)  
Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 359 GCTCCGCATCGTACTATGAAACAGTATCACTACTAAATGAATCTATTCTTGGATAGAA 418  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40

Db	419	TTTATAACTGAGAGGCATCTCGATATATGCTTACAAAAATCCACATTTGGATCTCTCAATTTTGAG	478
Qy	41	LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle	60
Db	479	AGGTACCACTCTATGTTTTTAAGGTTTCTGGAAGAACAAGCAGGCCAAAATGCCATA	538
Qy	61	TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe	80
Db	539	TGGATTGACTGTGGAATCCATGCCAGAGAATGGAATCTCTCTGCTTCTGCTGTGGTTC	598
Qy	81	IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle	100
Db	599	ATAGGCCATAATTCGAATGTGGAGAAAGACCGTTCTTTCTATGCGAACAAATCATTTGCATC	658
Qy	101	GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer	120
Db	659	GGAACAGACCTGAATAGAACTTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGT	718
Qy	121	SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla	140
Db	719	TCCTCATCTCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGCA	778
Qy	141	ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer	160
Db	779	GTGGCTAGTTTCTTTGAGAAGAAATATCAACCAGATTAAAGCATACATCAGCATGCATCA	838
Qy	161	TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu	180
Db	839	TACTCCAGCATATAGTGTGTTCATATTCCATATACAGAAAGTAAAGCAAGACCATGAG	898
Qy	181	GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr	200
Db	899	GAACGTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATTAGTAAAAATACC	958
Qy	201	ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspAsp	220
Db	959	AGGTATACATATGCGCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGACGAT	1018
Qy	221	TrpIleTyrAspLeuGlyIleLysTyrSerPhe-----	231
Db	1019	TGGATCTATGATTTGGCGATCAAAATATTCGTTTACAATTTGAATTCGAGATACGGGCACA	1078
Qy	232	-----ThrSerAsnProProValGluLysLeuLeuProLe	243
Db	1079	TACGGATTCTTGTCGCCGAGCGTTATACAAACCCACCTGTAGAGAAGCTTTTGCCGCT	1138
Qy	243	uSerLeuLys 246	
Db	1139	GTCTCTAAAA 1148	

## RESULT 2

US-08-869-057-1	
Sequence 1, Application US/08869057	
Patent No. 5985562	
GENERAL INFORMATION:	
APPLICANT: Morser, Michael J	
APPLICANT: Nagashima, MariKo	
TITLE OF INVENTION: Method of Detecting Thrombotic Disease	
TITLE OF INVENTION: Risk	
NUMBER OF SEQUENCES: 6	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Berlex Biosciences Legal Department	
STREET: 15049 San Pablo Avenue	
CITY: Richmond	
STATE: California	
COUNTRY: USA	
ZIP: 94804-0099	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: Patent In Release #1.0, Version #1.30	
CURRENT APPLICATION DATA:	



Db 763 CTGAATAGCAACTTTGCTTCCAAACACTGGTGTGAGGAAGTGCATCCATCTCTCATGC 822  
Qy 124 SerGluThrTy-CysGlyLeuTyProGluSerGluProGluVallylsAlaValAlaSer 143  
Db 823 TCGGAACCTACTGTGGACTTTTCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGT 882  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGln 163  
Db 883 TTCTTGAGGAAGAAATATCAACAGATTAAAGCATACATCAGCATGCTTTCATCTCCAG 942  
Qy 164 HisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 943 CATATAGTGTCTTCATATCTCTATACAGAACTTAAAGTAAAGCAAGACCATCAGGAAGTGTCT 1002  
Qy 184 LeuValAlaSerGluAlaValAlaGlnIleGluLysThrSerIleAsnThrArgTyThr 203  
Db 1003 CTAGTAGCAGTGAACGAGTGTCTTATTTGAAACCTAGTAAAGAAATACCAAGGTATACA 1062  
Qy 204 HisGlyHisGlySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTy 223  
Db 1063 CATGGCAGTGGCTCAGAACCTTATACCTAGCTCTCTGGAGTGGGGACGATTGGATCTAT 1122  
Qy 224 AspLeuGlyIleLysTySerPhe----- 231  
Db 1123 GATTTGGCATCAATATATCGTTTACAAATTGAACTTCGAGATACGGGCACATACGGATTC 1182  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuTy 246  
Db 1183 TTGCTGCGGAGCGTTTACATCAAAACCCACCTGTAGAGAAGCTTTTCCCGCTGTCTTAAA 1242  
Qy 246 s 246  
Db 1243 A 1243

RESULT 3

US-07-649-591B-2  
: Sequence 2, Application US/07649591B  
: Patent No. 5206161  
: GENERAL INFORMATION:  
: APPLICANT: Dennis Drayna and Daniel Eaton  
: TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 460 Point San Bruno Blvd  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: patin (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/649,591B  
: FILING DATE: 19910201  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Hasak, Janet E.  
: REGISTRATION NUMBER: 28,616  
: REFERENCE/DOCKET NUMBER: 689  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415/266-1896  
: TELEFAX: 415/952-9881  
: TELEX: 910/371-7168  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1749 bases  
: TYPE: NUCLEIC ACID

STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: hybridization probe  
LOCATION: 133 to 178  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: potential clip site  
LOCATION: 380 to 382  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: signal sequence  
LOCATION: 41 to 106  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-649-591B-2  
Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2  
US-09-980-881A-4 (1-246) x US-07-649-591B-2 (1-1749)  
Qy 1 AlaSerAlaSerTyTyGluGlnTyHisSerLeuAsnGluIleTySerTrpIleGlu 20  
Db 383 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAATCCCAATTTGGATTCCTCAITTTGAG 502  
Qy 41 LysTyProLeuTyValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AGTATCCCACTCTATGTTTAAAGGTTCCTGAAAAGAACAAACAGCCAAAATGCCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 563 TGGATTGACTGTGAATCCATGCCAGAGAATGGATCTCTCTGCTTTCTGCTTTGTGGTTTC 622  
Qy 81 IleGlyHis----- 83  
Db 623 ATAGGCCATATAACTCAATTCTATGGGATAATAGGCAATATACCAATCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTCTATGTTATGCCGGTGGTTAATGTGGACGGTTATGACTACTCATGGAAAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGAGAAAGAACCGTTCTTTCTATGCGAACCAATCATTCATCGCAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyValaSerSerSerCys 123  
Db 803 CTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCTATGC 862  
Qy 124 SerGluThrTy-CysGlyLeuTyProGluSerGluProGluVallylsAlaValAlaSer 143  
Db 863 TCGGAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGAGTGAAGCAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGln 163  
Db 923 TTCTTGAGGAAGAAATATCAACAGATTAAAGCATACATCAGCATGCTTTCATCTCCAG 982  
Qy 164 HisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTCTTCCATATTTCTTATACCAAGTAAAGCAAGACCATGAGGAACCTGTCT 1042

Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAACCCAGGTATACA 1102  
 Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTyr 223  
 Db 1103 CATGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 1162  
 Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
 Db 1163 GATTTGGGCATCAATAATTCTGTTTCAACTTGAACCTTCGAGATACGGGCACATACGGATTTC 1222  
 Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
 Db 1223 TTGCTGCCGGAGCGTTATCATCAACCCACCTGTAGAGAAGCTTTTGGCGGTGTCTCTAAA 1282  
 Qy 246 s 246  
 Db 1283 A 1283

RESULT 4

US-08-277-540-2  
 ; Sequence 2, Application US/08277540  
 ; Patent No. 5474901  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
 ; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/277,540  
 FILING DATE: 19-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/167727  
 FILING DATE: 15-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/959944  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/649591  
 FILING DATE: 01-FEB-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 689D1C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1749 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

Alignment Scores:

Pred. No.: 7,12e-154 Length: 1749  
 Score: 1272.00 Matches: 246  
 Percent Similarity: 81.73% Conservative: 0

Best Local Similarity: 81.73% Mismatches: 0  
 Query Match: 95.07% Indels: 55  
 DB: 1 Gaps: 2  
 US-09-980-881A-4 (1-246) x US-08-277-540-2 (1-1749)  
 Qy 1 AlaserAlaserTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTyrIleGlu 20  
 Db 383 GCCTCCCGCATCGTACTATGAACAGTATCACTCAATAAATAAATCTATCTTTGGATGAA 442  
 Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
 Db 443 TTATAACTGAGAGCATCCTGATATGCTTACAAAATCCACATTTGGATCTCTATTGAG 502  
 Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
 Db 503 AAGTACCACCTCTATGTTTAAAGGTTTCTGGAAAAGAACAAACAGCAAAATGCCATA 562  
 Qy 61 TrpIleAspCysGlyIleHisAlaAtqGluTyrPheSerProAlaPheCysLeuTyrPhe 80  
 Db 563 TGGATTGACTGTGAATCCATGCCAGAGATGGATCTCTCTCTCTTTCTGCTTTGTTGTTT 622  
 Qy 81 IleGlyHis----- 83  
 Db 623 ATAGCCCATATACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTCTGAGGTT 682  
 Qy 83 ----- 83  
 Db 683 GTGGATTCTTATGTTATGCCGGTGTAAATGTGGACGGTTATGACTACTCATGGAATAAG 742  
 Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
 Db 743 AATCGAATGTGGAAAAGAACCGTTCTTTCTATCGCAACAATCAATCATCGGAACAGAC 802  
 Qy 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlyAlaLaserSerSerCys 123  
 Db 803 CTGNAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCTCATGC 862  
 Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
 Db 863 TCGGAAACCTACTGTGGACTTTATCTGAGTCAGAACAGAGTGAAGGCGAGTGGCTAGT 922  
 Qy 144 PheLeuArgArgAsnIleAsnGlnIleValAlaTyrIleSerMetHisSerTyrSerGln 163  
 Db 923 TCTTGAGAGAAATATCAACAGATTAAGATACATACATCAGCATGCAATTCATCTCCAG 982  
 Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
 Db 983 CATATAGTGTTCATATTCCTATACACGAAGTAAAGCAAAAGACCATGAGGAACCTGTCT 1042  
 Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAACTAGTAAATAAATACCCAGGTATACA 1102  
 Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTyrIleTyr 223  
 Db 1103 CATGCCATGGCTCAGAAACCTTATACCTAGCTCCTGGAGGTGGGACGATTGGATCTAT 1162  
 Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
 Db 1163 GATTTGGGCATCAATAATTCTGTTTCAACTTGAACCTTCGAGATACGGGCACATACGGATTTC 1222  
 Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
 Db 1223 TTGCTGCCGGAGCGTTATCATCAACCCACCTGTAGAGAAGCTTTTGGCGGTGTCTCTAAA 1282  
 Qy 246 s 246  
 Db 1283 A 1283  
 RESULT 5  
 US-08-430-787A-2  
 ; Sequence 2, Application US/08430787A

Patent No. 5593674  
GENERAL INFORMATION:  
APPLICANT: Drayna, Dennis T., Eaton, Dan L.  
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,787A  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,540  
FILING DATE: 19-JUL-1994  
APPLICATION NUMBER: 08/167727  
FILING DATE: 15-DEC-1993  
PRIOR APPLICATION DATA: 07/959944  
FILING DATE: 14-OCT-1992  
APPLICATION NUMBER: 07/649591  
FILING DATE: 01-FEB-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 689D1C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1749 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-430-787A-2

Alignment Scores:  
Pred. No.: 7,12e-154 Length: 1749  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 1 Gaps: 2

US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20  
Db 383 GCCTCCGACGCTACTATGACAGTATCACTCACTAAATGAATCTATTCTTGGATAGAA 442  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40  
Db 443 TTTTATACTCAGAGGCACTCTGTATGCTTTACAAAAATCCACATTTGGATCTCTATTGAG 502  
Qy 41 LysTyrProLeuTyrValLeuValSerGlyIleGluGlnThrAlaLysAsnAlaIle 60  
Db 503 AAGTACCCTCTATGTTTAAAGGTTCTGGAAGAACAAACAGCCAAAATGCCATA 562  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 563 TGGATTGACTGTGAATCCATGCCAGAGATGGATCTCTCTCTTCTCTTGTGTGTTTC 622

Qy 81 IleGlyHis----- 83  
Db 623 ATAGCCATATAACTCAATTTCTATGGGATAATAGGCAATATACCAATCTCTCTGAGGCTT 682  
Qy 83 ----- 83  
Db 683 GTGGATTTCTATATCCCGTGGTAAATGTGGACGGTTATGTACTCTCATGGAAAAAG 742  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 743 AATCGAATGTGGAGAAAGAACCGTTCTTTCTATGGCAACAATCATTTGATCGGAACAGAC 802  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGlyAlaSerSerSerSerCys 123  
Db 803 CTGATATAGGAACCTTTGCTTCCAAACACCTGGTGTAGGAAGGTGCTATCAGTTCTCTATGC 862  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaLaser 143  
Db 863 TCGGAACCTTACTGTGGACTTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGCTAGT 922  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 923 TTCCTTGAAGAAGAAATATCAACCGATTAAAGCATACATCAGCATGCAATTCATCTCCCAG 982  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 983 CATATAGTGTTCATATTTCTATACAGAGTAAAGCAAGAACCATGAGGAACCTGTCT 1042  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1043 CTAGTAGCCAGTGAAGCAGTTCGTCTATTGAGAAAACTAGTAAAAAATACACAGGTATACA 1102  
Qy 204 HisGlyHisGlySerGluThrLeuAlaProGlyGlyLysAspAspTrpIleTyr 223  
Db 1103 CATGCCATGGCTCAGAAACCTTATACCTAGTCTCTGGAGGTGGGACGATTGGATCTAT 1162  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1163 GATTTGGGCATCAATATTCGTTTACAAATTTGAGATACGGGCACATACGGATTTC 1222  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1223 TTGCTGCCGAGCGTTATACATCAACCCACCTGTAGAGAAGCTTTTGGCCGCTGTCTCTAAA 1282  
Qy 246 s 246  
Db 1283 A 1283

RESULT 6

US-08-782-760-5  
Sequence S, Application US/08782760  
Patent No. 5948668  
GENERAL INFORMATION:  
APPLICANT: Hartman, Jacob  
APPLICANT: Fulga, Netta  
APPLICANT: Mendelovitch, Simona  
APPLICANT: Gorecki, Marian  
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE  
TITLE OF INVENTION: CARBOXYPEPTIDASE B  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,760
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,233
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; US-08-782-760-5

Alignment Scores:
Pred. No.: 8,48e-69 Length: 927
Score: 610.00 Matches: 126
Percent Similarity: 60.50% Conservative: 44
Best Local Similarity: 44.84% Mismatches: 71
Query Match: 45.59% Indels: 41
DB: 2 Gaps: 5

US-09-980-881a-4 (1-246) x US-08-782-760-5 (1-927)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GCAAGTGACACAGCATACCAAGTACCAACCACTGGGAACGATTGAGCGCTGGATTCAA 60

Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 CAAGTGGCCATGATATCCAGACCTTGCTACTCAGAGCGTCATTGGAAACCACTTTGAA 120

Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 GGACGTAACATGATGCTCTCAAGATT--GGTAAACATAGACCCGGAATAAGCCTGCCATC 177

Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 TTCATCGATTGGTGTTCCTCCAGAGAGATGGATTCTCTCGCATTCGTGACGTGGTTT 237

Qy 81 Ile----- 81
Db :

Qy 238 GTGAGAGAGGCTGTCCTGATCTATTAATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297
Db :

Qy 82 -----GlyHis----- 83
Db :

Qy 298 CTGGATTCTATGTTCTGCTGTCACCATGATGCTATGCTACACCTGGACTAAG 357
Db :

Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
358 GACAGAAATGTGGAGAAAACCGCTCTACTATGCTGGAAGTTCCTGCTGGGTGTAGAC 417

Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 CCCAACGAATTTT---AATGCTGGCTGGTGTGAAGTGGGAGCTTCTCGGAGTCCCTGC 474

Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
475 TCTGAAACTTACTGTGGACACGCCGCCAGAGTCTGAAAAAGACACAAAGGCCCTTGGCAGAT 534

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Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
535 TTCATCGCAACCAACCTCTCCACCATCAGGCTTACCTGACCATCCACTCATATCTACAG 594

Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
595 ATGATGCTCTACCTTACTCTATGACTACAAACTGCCTGAGAACTATGAGGAATTGAAT 654

Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
655 GCCTGTGTGAAGGTGGCAAGAGAGCTT--GCCACTCTGCATGCGCACCAAGTACACA 711

Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 TATGGCCAGGAGCTACAACTATCTCTGCTGCTGGGGATCTGACGACTGCTCTTAT 771

Qy 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProValGluLysLeuLeuProLeu 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
772 GATCAGGAATCAAAATATCTTACCTTTGAACT-CCGGGATACAGGCTTCTTTGGCTT 830

Qy 244 Ser 244
Db |||||
831 TCT 833

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RESULT 7
PCT-US96-00995-5
; Sequence 5, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; PCT-US96-00995-5

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Alignment Scores:
Pred. No.: 8,48e-69 Length: 927
Score: 610.00 Matches: 126

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Percent Similarity: 60.50% Conservative: 44  
 Best Local Similarity: 44.84% Mismatches: 71  
 Query Match: 45.59% Indels: 41  
 DB: 5 Gaps: 5

US-09-980-881A-4 (1-246) x PCT-US96-00995-5 (1-927)

QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20  
 DB 1 GCAAGTGGACACAGCTACACCAAGTACACAACTCGGAAACGATTGAGCGGTGGATTCAA 60  
 QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
 DB 61 CRAAGTGGCACTGATAATCCAGACCTTGCTCACTCAGAGCGCTCATTTGGAAACCAATTTGAA 120  
 QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
 DB 121 GCGAGTAACATGATGCTCTCAAGATT---GGTAAAACTAGAGACCGAATAAGCGCTCCATC 177  
 QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
 DB 178 TTCTCATGATTGGTGTTCCTCAAGAGAGAGTGGATTTCCTCGCATTCGTCAGTGGTTT 237  
 QY 81 Ile----- 81  
 DB 238 GTGAGAGAGCTGTCGTACTTATAATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297  
 QY 82 -----GlyHis----- 83  
 DB 298 CTGATTTCATGTTCTGCTGCTGGTCAACATTGATGCTGTCTACACCTGGACTAAG 357  
 QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
 DB 358 GACAGAATGTGAGAAAAACCGCTCTACTATGCTGGTGAAGTCTCTGCTGGGTGTAGAC 417  
 QY 104 LeuAsnArgAspPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
 DB 418 CCCAACAGGAATTTT---AATGCTGGCTGCTGTGAAGTGGAGCTCTCGAGTCCCTGC 474  
 QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaSer 143  
 DB 475 TCTGAACCTTACTGTGGACCGCCAGAGTCTGAAAGAGACAAAGGCCCTGGCAGAT 534  
 QY 144 PheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
 DB 535 TTATCCGCAACAACTCTCCACCATCAAGGGCTACTGACCATCCACTCATACTCACAG 594  
 QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuLeuSer 183  
 DB 595 ATGATGCTCTACCTTACTCTTATGACTACAACTGCTGAGAACTATAGGAATTTGAT 654  
 QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
 DB 655 GCCCTGGTGAAGGTCGGCAAGGAGCTT---GCCACTCTGCTGATGGCAACCAAGTACACA 711  
 QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
 DB 712 TATGGCCAGGAGCTACAAATCTATCTGCTGCTGGGGGATCTGACGACTGGCTTAT 771  
 QY 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProValGluLysLeuProLeu 243  
 DB 772 GATCAGGAATCAATATTCTTTTACCTTTTGAACCT-CCGGGATACAGGCTTCTTTGGCTT 830  
 QY 244 Ser 244  
 DB 831 TCT 833

RESULT 8

US-08-696-139-3  
 ; Sequence 3, Application US/08696139  
 ; Patent No. 5672496  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fayerman, Jeffrey T.

APPLICANT: Greenen, David P.  
 APPLICANT: Hersberger, Charles L.  
 APPLICANT: Larson, Jeffrey L.  
 APPLICANT: Sterner, Jane L.  
 APPLICANT: Zhang, Haichao  
 TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE  
 TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Eli Lilly and Company  
 STREET: Lilly Corporate Center  
 CITY: Indianapolis  
 STATE: Indiana  
 COUNTRY: United States of America  
 ZIP: 46285  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/696.139  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/153,258  
 FILING DATE: 16-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-8681  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 921 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..921  
 US-08-696-139-3

Alignment Scores:  
 Pred. No.: 3,48e-65 Length: 921  
 Score: 582.00 Matches: 117  
 Percent Similarity: 59.47% Conservative: 40  
 Best Local Similarity: 44.32% Mismatches: 67  
 Query Match: 43.50% Indels: 40  
 DB: 1 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-696-139-3 (1-921)

QY 6 TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg 25  
 DB 16 TATGAAGTACAACTGGAACGATCGAGGCTTGACATGACAGTACAGTCAAGTAA 75  
 QY 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45  
 DB 76 AATCCAGACCTCATCTCTCGACAGCCATCGGAACATACATTTTAGGAAACAATATATAC 135  
 QY 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65  
 DB 136 CTCCTCAAGTT---GGCAAACTGGACCAAAATAGCTCGCATTTTCATGGACTGTGGT 192  
 QY 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81  
 DB 193 TTCCATGCCAGAAATGGATTTCCTCCATTTTCCAGTGGTTTGTGTGAGAGAGGCTGTT 252  
 QY 81 ----- 81

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Db 253 CTCACCTATGATATGAGAGTCACATGACAGAAATTCCTCAACAAGCTAGACTTTTATGTC 312
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88
Db 313 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGA 372
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 373 AAGACCCGCTCTCAATGCTGGAACTACCTGGCAATGGCACAGACCCCAACAGAAATTTT 432
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTrpCys 128
Db 433 ---GATGCTGGTGGTGACAACTGGAGCCTCTACAGACCCCTGGATGAGACTACTGT 489
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 490 GGATCTGCTGCAGAGTCTGAAAGAGACCAAGCCCTGGCTGATTTTATACGCAACAC 549
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 550 CTCCTCTCCATCAAGACATACCTGACGATCCACTCATACTACAGATGATACTCTACCC 609
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 610 TATTCCTATGATTACAACTCCCGAGAACAAATGCTGAGTTGAATACCTGGCTAAGCT 669
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 670 GCGGTGAAGAACTT---GCTACACTGTATGGCACCAAGTACATACATACGGGCCAGGAGCT 726
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyClyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 727 ACAACAAATCTATCTGCTGCTGGGGGCTCTGATGACTGGGCTTATGACCAAGGAATCAA 786
Qy 229 TyrSerPheThr 232
Db 787 TATTCCTTCACC 798

RESULT 9
US-08-696-139-1
; Sequence 1, Application US/08696139
; Patent No 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hershenberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Sterner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1215
; US-08-696-139-1

Alignment Scores:
Pred. No.: 5,49e-65 Length: 1215
Score: 582.00 Matches: 117
Percent Similarity: 59.47% Conservative: 40
Best Local Similarity: 44.32% Mismatches: 67
Query Match: 43.50% Indels: 40
DB: Gaps: 5

US-09-980-881A-4 (1-246) x US-08-696-139-1 (1-1215)
Qy 6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
Db 310 TATGAGAAGTACAACAACATCGGAACGATCGAGCTTGGACTAAGCAAGTCACCAAGTAA 369
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 370 AATCCAGACCTCATCTCTCGCACAGCCATCGGAACATCATATTTTAGAAGAACATATATAC 429
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 430 CTCCTCAAGTT---GGCAACCTGGACCAATAAGCTGCCATTTTCATGGACTGTGGT 486
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 487 TTCCATGCCAGAGAATGGATTTCCTCATGCTTTTCCATGCTTTTGCAGTGGTTTGTGAGAGAGGCTGTT 546
Qy 81 ----- 81
Db 547 CTCACCTATGATATGAGAGTCACATGACAGAAATTCCTCAACAAGCTAGACTTTTATGTC 606
Qy 82 -----GlyHis-----AsnArgMetTrpArg 88
Db 607 TTGCCTGTGCTCAATATTGATGGCTACATCTACACCTGGACCAAGAACCGAATGTGGAGA 666
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 667 AAGACCCGCTCTACCAATGCTGGAACTACCTGCAATGGCACAGACCCCAACAGAAATTTT 726
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCys 128
Db 727 ---GATGCTGGTGGTGACAACTGGAGCCCTCTACAGACCCCTGGATGAGACTTACTGT 783
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 784 GGATCTGCTGCAGAGTCTGAAAGAGACCAAGCCCTGGCTGATTTTATACGCAACAC 843
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 844 CTCCTCTCCATCAAGACATACCTGACGATCCACTCATACTACAGATGATACTCTACCC 903
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 904 TATTCCTATGATTACAAACTCCCGAGAACAAATGCTGAGTTGAATAACCTGGCTAAGCT 963
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
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Thu Oct 28 07:16:17 2004

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-860-882A-64

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-64 (1-1053)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGAAACGATAGAGCTTGGACTCAA 126
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAAGTCCCACTCAGAAATCAGCCCTCATCTCCGACGTGTATCGGAACCAATTTGAG 186
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCTATTACCTCTGAAGGTT--GGCAAGCTGGACAAAATTAAGCTGCCATT 243
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTyrPheSerProAlaPheCysLeuTrpPhe 80
DB 244 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGATTTCTCTGTCATTTGCCAGTGGTTT 303
QY 81 Ile-----GlyHis----- 81
DB 304 GTAAGAGAGCTGTTCTGATCTTACCTATGGACGTGATCCAAGTGACAGAGCTTCTCGACAAG 363
QY 82 -----GlyHis----- 83
DB 364 TTAGACTTTTATGCTCTGCTGCTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 423
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCATACTGGATCTAGCTGGCATTTGCCACAGAC 483
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 484 CCCAACAGAAATTTT---GATGCTGGTGTGTGTAATTTGGAGCCTCTCGAAACCCCTGT 540
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 541 GATGAACTTACTGTGGACCTGCCGAGAGTCTGAAAGGAGAGACCAAGGCCCTGGCTGAT 600
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 601 TTCATCGCAACAACACTCTCTTCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 660
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 661 ATGATGATCTACCCCTTACTCATATGCTTCAAACTCGGTGAGAACAAATGCTGAGTTGAAI 720
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 721 GCCCTGGCTAAAGTACTGTGAAGAAGTCTT---GCCTCCTGACGCGCACCAAGTACACA 777
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyr 223
DB 778 TATGCCCGGAGCTACAACAATCTATCTGCTGCTGGGGCTCTGACGACTGGCTTAT 837
QY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 838 GACCAAGGAATTCAGATATTCCTTACC 864

RESULT 13
US-09-011-769A-46
; Sequence 46, Application US/09011769A
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; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01975
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9612295.7
; FILING DATE: 12-JUN-1996
; APPLICATION NUMBER: GB 9611019.2
; FILING DATE: 25-MAY-1996
; APPLICATION NUMBER: GB 9516810.0
; FILING DATE: 16-AUG-1995
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1053 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1047
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..1047
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-011-769A-46

Alignment Scores:
Pred. No.: 3,76e-63 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-46 (1-1053)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 67 GCAACTGGTCACTCTTACGAGAAGTACAACAAGTGGAAACGATAGAGCTTGGACTCAA 126
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAAGTCCCACTCAGAAATCAGCCCTCATCTCCGACGTGTATCGGAACCAATTTGAG 186
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCTATTACCTCTGAAGGTT--GGCAAGCTGGACAAAATTAAGCTGCCATT 243
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Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 244 TTCATGGAGCTGTGGTTTCCAGCCAGAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 303
Qy 81 Ile----- 81
Db 304 GTAAGAGAGGCTGTTTCGTACCTATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAA 363
Qy 82 -----GlyHis----- 83
Db 364 TTAGACTTTTATGCTCCTGCTGCTCAATATGATGCTACATCTACACCTGGACCAAG 423
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyraAlaAsnAsnHisCysIleGlyThrAsp 103
Db 424 AGCCGATTTTGGAGAAAGACTCGCTCCACCATATCTGGATCTAGCTGCAATGGCACAGAC 483
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 484 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAATTTGGAGCTCTCGAAACCCCTGT 540
Qy 124 SerGluThrTyrcysGlyLeuTyrrProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATGAACCTTACTGTGGACCTGCCGACAGTCTGAAAGAGAGACCAAGGCCCTGGCTGAT 600
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGln 163
Db 601 TTCATCCGCAACAACCTCTCTCCATCAAGGCATATCTGACAAATCCACTCGTACTCTCCAA 660
Qy 164 HisIleValPheProTyrrSerTyrrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 661 ATGATGATCTACCTTACTATATCTTACAACTCGGTGAGAACATGCTGAGTTGAT 720
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrrThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAGAACTT---GCCTCACTGCACGGCACCAAGTACACA 777
Qy 204 HisGlyHisGlySerGluThrLeuTyrrLeuAlaProGlyGlyAspAspTrpIleTyrr 223
Db 778 TATGCCCGGAGCTACAAACATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 837
Qy 224 AspLeuGlyIleLysTyrrSerPheThr 232
Db 838 GACCAAGGAATCAGATATCTCTTACC 864
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## RESULT 14

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US-08-860-882A-56
; Sequence 56, Application US/08860882A
; Patent No 5985281
; GENERAL INFORMATION:
; APPLICANT: TAYLORSON, CHRISTOPHER JOHN
; APPLICANT: EGGELTE, HENDRIKUS JOHANNES
; APPLICANT: TARRAGONA-FIOL, ANTONIO
; APPLICANT: RABIN, BRIAN ROBERT
; APPLICANT: BOYLE, FRANCIS THOMAS
; APPLICANT: HENNAW, JOHN FREDERICK
; APPLICANT: BLAKELY, DAVID CHARLES
; APPLICANT: MARSHAM, PETER ROBERT
; APPLICANT: HEATON, DAVID WILLIAM
; APPLICANT: DAVIES, DAVID HUW
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESS: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/860,882A
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; FILING DATE: JUNE 23, 1997
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; CLASSIFICATION: 424
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; ATTORNEY/AGENT INFORMATION:
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```
; NAME: DONALD J. BIRD
```

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; REGISTRATION NUMBER: 25,323
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; REFERENCE/DOCKET NUMBER: 9901/238653
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (202) 861-3027
```

```
; TELEFAX: (202) 822-0944
```

```
; TELEX: 6174627 CUSH
```

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; INFORMATION FOR SEQ ID NO: 56:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1263 bases
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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; TOPOLOGY: linear
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US-08-860-882A-56
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## Alignment Scores:

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Pred. No.: 5,08e-63 Length: 1263
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5
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US-09-980-881A-4 (1-246) x US-08-860-882A-56 (1-1263)
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Qy 1 AlaSerIleSerTyrrTyrrGluGluGluTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGlu 20
Db 325 GCAACAGACACAGATTTATGAGAGTACACAAAGTGGGAAACGATAGAGGCTTGACCTCAA 384
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 385 CAAGTCCCACTGAGATCCAGCCCTCATCTCTCGCAGTGTATCGGAACACCATTTGAG 444
Qy 41 LysTyrrProLeuTyrrValLeuLysValSerGlyLysGluGluGluThrAlaLysAsnAlaIle 60
Db 445 GGACGCGCTATTACCTCTCTGAAAGTT---GGCAAGCTGGACAAATAAGCCTGCCATTT 501
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 502 TTCATGGAGCTGTGGTTTCCATGCGCAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 561
Qy 81 Ile----- 81
Db 562 GTAAGAGAGGCTGTTTCGTACCTATGGACGTGAGATCCAAAGTGACAGAGCTTCTCGACAA 621
Qy 82 -----GlyHis----- 83
Db 622 TTAGACTTTTATGCTCCTGCTGCTCAATATGATGGCTACATCTACACCTGGACCAAG 681
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyraAlaAsnAsnHisCysIleGlyThrAsp 103
Db 682 AGCCGATTTTGGAGAAAGACTCGCTCCACCATATCTGGATCTAGCTGCAATGGCACAGAC 741
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 742 CCCAACAGAAATTTT---GATGCTGGTTGGTGTGAATTTGGAGCTCTCGAAACCCCTGT 798
Qy 124 SerGluThrTyrcysGlyLeuTyrrProGluSerGluProGluValLysAlaValAlaSer 143
Db 799 GATGAACCTTACTGTGGACCTGCCGACAGTCTGAAAGAGAGACCAAGGCCCTGGCTGAT 858
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrrIleSerMetHisSerTyrrSerGln 163
Db 859 TTCATCCGCAACAACCTCTCTCCATCAAGGCATATCTGACAAATCCACTCGTACTCTCAA 918
Qy 164 HisIleValPheProTyrrSerTyrrThrArgSerLysSerLysAspHisGluLeuSer 183
Db 919 ----- 943
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Db 919 ATGATGATACCTTACTCATATGCTTACAAACTCGGTGAGAACAACTGCTGAGTTGAAT 978  
Qy 184 LeuValAlaSerGluAlaValargAlaLleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 979 GCGCTGGCTAAAGCTACTGTGAAGAAGACTT---GCCCTCACTGCACGGCACCAGTACACA 1035  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 223  
Db 1036 TATGGCCGGAGCTACACAATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 1095  
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232  
Db 1096 GACCAAGGAATCAGATATTCCTTCACC 1122

RESULT 15  
US-09-011-769A-38  
; Sequence 38, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKLEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAM, Peter R.  
; DOWELL, Robert I.  
; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011,769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1263 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-011-769A-38  
  
Alignment Scores:  
Pred. No.: 5.08e-63 Length: 1263  
Score: 567.00 Matches: 111  
Percent Similarity: 58.36% Conservative: 46  
Best Local Similarity: 41.26% Mismatches: 72  
Query Match: 42.38% Indels: 40  
DB: 4 Gaps: 5  
  
US-09-980-881A-4 (1-246) x US-09-011-769A-38 (1-1263)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluLleTyrSerTrpIleGlu 20  
Db 325 GCAACAGGACACAGCTTATGAGAGTACAAACAAAGTGGGAAACGATAGAGGCTTGGACTCAA 384  
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 385 CAAGTCGCCACTGAGATCCAGCCCTCATCTCTCGAGTGTATCGGAACCCACCATTTGAG 444  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 445 GGACGCGCTATTACCTCCTCAAGTT---GGCAAGCTGGACAAATAAGCTGCCATT 501  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 502 TTCATGGACTGTGGTTTCCATGCCAGAGAGTGGATTTCTCTGCAATTCGCCAGTGGTTT 561  
Qy 81 Ile----- 81  
Db 562 GTAAGAGAGGCTGTTGCTGATGAGCTGAGATCCAAAGTGCAGAGCTTCTCGACAAG 621  
Qy 82 -----GlyHis----- 83  
Db 622 TTAGACTTTTATGTCCTGCTGCTCAATATTGATGGCTACATCTACACCTGGACCAAG 681  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 682 AGCCGATTTTGGAGAAAGACTCGCTCCACCCTACTGATCTAGCTGCAATTTGGCACAGAC 741  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 742 CCCAACAGAAATTTT---GATGCTGGTGGTGTGAAATTTGGAGCCTCTCGAAACCCCTGT 798  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 799 GATGAACCTTACTGTGGACCTGCCACAGCTGAAAAGAGAAACCAAGCCCTGGCTGAT 858  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 859 TTCATCCGCACAAACTCTCTTCCATCAAGGCATATCTGACAATCCACTCGTACTCCCAA 918  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 919 ATGATGATCTACCCCTTACTCATATGCTTACAAACTCGGTGAGAACAAATCTGAGTTGAAT 978  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
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Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyr 223  
Db 1036 TATGGCCGGAGCTACACAATCTATCTCTGCTGGGGGCTCTGACGACTGGGCTTAT 1095  
Qy 224 AspLeuGlyIleLysTyrSerPheThr 232  
Db 1096 GACCAAGGAATCAGATATTCCTTCACC 1122

Search completed: October 27, 2004, 02:01:25  
Job time : 71.6271 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: October 27, 2004, 01:54:23 ; Search time 1178.4 Seconds  
(without alignments)  
1070.424 Million cell updates/sec

Title: US-09-980-881A-4  
Perfect score: 1338  
Sequence: 1 ASASYEQYHSLNEIYSWIE.....IKYSFTSPNPVKKLPLSLK 246

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0980881@cgn\_1\_1034\_@runat\_26102004\_084115\_7269  
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Database : Published Applications NA:  
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8: /cgnt2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgnt2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgnt2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgnt2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
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15: /cgnt2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
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19: /cgnt2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
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21: /cgnt2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Alignment Scores:

Result No.	Score	Query Match	Length	DB ID	Description
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3	1272	95.1	1728	9	US-09-880-107-2396
4	1248.5	93.3	1344	16	US-10-115-479-69
5	1248.5	93.3	1743	16	US-10-115-479-67
6	1177	88.0	1272	15	US-10-379-836-1
7	902	67.4	1400	9	US-09-925-302-24
8	902	67.4	1400	10	US-09-925-302-24
9	869.5	65.0	1037	16	US-10-115-479-63
10	830.5	62.1	1132	16	US-10-115-479-65
11	556.5	41.6	1302	17	US-10-477-515-1
12	556.5	41.6	1311	13	US-10-200-344-9
13	556.5	41.6	1993	15	US-10-274-639-33
14	556.5	41.6	1993	16	US-10-333-574-33
15	554.5	41.4	1907	18	US-10-757-262-127
16	552	41.3	1254	14	US-10-229-546-3
17	552	41.3	1622	14	US-10-229-546-1
18	552	41.3	1622	15	US-10-429-802-21
19	552	41.3	1622	16	US-10-430-503-12
20	552	41.3	1622	16	US-10-262-511-71
21	552	41.3	1622	16	US-10-641-643-1020
22	552	41.3	1633	15	US-10-341-434-187
23	552	41.3	1740	14	US-10-116-802-95
24	550.5	41.1	1125	9	US-09-888-615-2
25	550.5	41.1	1332	15	US-10-176-306-75
26	550.5	41.1	1603	15	US-10-176-306-73
27	549	41.0	1870	9	US-09-910-059-112
28	549	41.0	1870	17	US-10-608-710-3
29	549	41.0	2154	9	US-09-910-059-124
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32	533.5	39.9	991	16	US-10-383-201-93
33	525.5	39.3	2128	13	US-10-200-344-13
34	523.5	39.1	1295	17	US-10-363-829-148
35	492	36.8	1200	14	US-10-200-910-7
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37	471.5	35.2	1050	13	US-10-200-344-11
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40	465.5	34.8	1260	16	US-10-257-174-16
41	465.5	34.8	1279	16	US-10-236-417-217
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44	465.5	34.8	1311	16	US-10-257-174-15
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ALIGNMENTS

RESULT 1  
US-09-813-133A-1  
; Sequence 1, Application US/09813133A  
; Publication No. US20020137179A1  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1625  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-1

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Pred. No.: 1.39e-159 Length: 1625
Score: 1289.50 Matches: 244
Percent Similarity: 92.42% Conservative: 0
Best Local Similarity: 92.42% Mismatches: 2
Query Match: 96.38% Indels: 18
DB: 9 Gaps: 1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 359 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAAATCTATTCTTGATAGAA 418
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 419 TTTATAACTGAGAGCATCTGATATGCTTCAAAAATCCCAATTCGATCCTCATTTGAG 478
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 479 AAGTACCCACTCTATGTTTAAAGGTTTCTGAAAAGAACAGCAGCCAAAATGCCCATA 538
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 539 TGGATTGACTGTGGAATCCATGCCAGAGATGGAATCTCTCTGCTTCTGCTGGTTC 598
Qy 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIle 100
Db 599 ATAGGCCATAATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACATCATTTGATC 658
Qy 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
Db 659 GGAACAGACCTGAATAGGAACCTTTGCTTCCAAACACTGGTGTGAGGAGGTGCATCCAGT 718
Qy 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValIleAla 140
Db 719 TCCTCATGCTCGAAACCTACTGTGGACTTTATCCTGAGTCAGAACCCAGAGTGAAGGCA 778
Qy 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
Db 779 GTGGTAGTTTCTTGAGAGAAATATCAACAGATTAAAGCAATACATCAGCATGCAATCA 838
Qy 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
Db 839 TACTCCAGCATATAGTGTTCATATTCCTATACAGAAATTAAGCAAGAACCATGAG 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACTGTCTAGTAGCCAGTGAAGCAGTTCTGCTGCTATTGAGAAAATTAGTAAAAATACC 958
Qy 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAsp 220
Db 959 AAGTATACATATGGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGAT 1018
Qy 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe 231
Db 1019 TGGATCTATGATTTGGGCATCAAAATATTCGTTTTACAATTTGAACCTTCGAGATCGGGCACA 1078
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 1079 TACGATTTCTGTCGGCGGCGTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAA 1148

RESULT 2
US-10-212-877-1
; Sequence 1, Application US/10212877
; Publication No. US20030017574A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
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; TITLE OF INVENTION: USBS THEREOF
; FILE REFERENCE: C1001173DIV
; CURRENT APPLICATION NUMBER: US/10/212,877
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/813,133
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-877-1
```

```
Alignment Scores: 1.39e-159 Length: 1625
Pred. No.: 1289.50 Matches: 244
Score: 1289.50 Matches: 244
Percent Similarity: 92.42% Conservative: 0
Best Local Similarity: 92.42% Mismatches: 2
Query Match: 96.38% Indels: 18
DB: 9 Gaps: 1
```

US-09-980-881A-4 (1-246) x US-10-212-877-1 (1-1625)

Db 1079 TACGATTTCTGCTCCGCGGCTTACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 1138  
Qy 243 uSerLeuLys 246  
Db 1139 GTCTCTAAAA 1148

RESULT 3

US-09-880-107-2396  
; Sequence 2396, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2396  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M75106  
US-09-880-107-2396

Alignment Scores:

Pred. No.: 3,17e-157 Length: 1728  
Score: 1272.00 Matches: 246  
Percent Similarity: 81.73% Conservative: 0  
Best Local Similarity: 81.73% Mismatches: 0  
Query Match: 95.07% Indels: 55  
DB: 9 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-880-107-2396 (1-1728)

Qy 1 AlaSerAlaSerTyrTrpGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGlu 20  
Db 362 GCCTCGGCATCGTACTATGAACAGTATCACTCAATAATGAAATCTATTCTTGGATAGAA 421  
Qy 21 PheIleThrGluArgHisProaspMetLeuThrLysIleHisIleGlySerSerPheGlu 40  
Db 422 TTTATTAACGTGAGAGGCATCTGTATGCTTTACAAAATCAACATTTGGATCCTCATTTGAG 481  
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60  
Db 482 AAGTACCCACTCATGTTTAAAGGTTCTGGAAGAGAACAAACAGCCAAATGCCATA 541  
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80  
Db 542 TGGATTGACTGTGGAATCCATGTCAGAGAATGGATCTCTCTGCTTTCTGCTTTGTTGTTTC 601  
Qy 81 IleGlyHis----- 83  
Db 602 ATAGGCCATATACTCAATTTCTATGGATTAATAGGCAATATACCAATCTCTGAGGCTT 661  
Qy 83 ----- 83  
Db 662 GTGATTTCTATGTTATGCGGTTGTTAATGTGACGGTTTATGACTACTCATCGAAAAAG 721  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 722 AATCGAATGTGGAGAAAGACCGTTCTTTCTATGCGAACAAATCATTTGCATCGGAACAGAC 781  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123

Db 782 CTGAATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGC 841  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValValAlaValAlaSer 143  
Db 842 TCGGAAACCTTACTGTGGACTTTTATCTCGATCAGAACCCAGAGTGAAGCCAGTGGCTAGT 901  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 902 TTTCTTGAGAGAATATCAACACAGATTAAAGCATACATCAGCATGCATTCATCTCCAG 961  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 962 CATATAGTGTTCATATTTCTATACAGAAAGTAAAGCAAGCAAGCCATGAGGAACCTGTCT 1021  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1022 CTAGTAGCCAGTGAAGCAGTTCTGCTATTGAGAAACTAGTAAATAATACAGGTATACA 1081  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspTrpIleTyr 223  
Db 1082 CATGCCATGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGGGACGATTGGATCTAT 1141  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1142 GATTGGGCATCAAAATATTCTGTTTACAATTGAACTTCGAGATACGGGCACATACGATTC 1201  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1202 TTGTCGCGGAGCGTTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGCTGTCTCTAAA 1261  
Qy 246 s 246  
Db 1262 A 1262

RESULT 4

US-10-115-479-69  
; Sequence 69, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:

; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shalomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03

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; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 69
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1315)
US-10-115-479-69

Alignment Scores:
Pred. No.:      2,71e-154      Length:      1344
Score:          1248.50      Matches:      244
Percent Similarity: 79.74%      Conservative: 0
Best Local Similarity: 79.74%      Mismatches: 2
Query Match:      93.31%      Indels:      60
DB:              16      Gaps:      3

US-09-980-881A-4 (1-246) x US-10-115-479-69 (1-1344)

Qy      1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db      373 GCCTCCGCATCGTACTATGAACAGTATCACTCACTAAATGAATCTATCTTGATAGAA 432
Qy      21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db      433 TTTATACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTTGGATCCTCATTTGAG 492
Qy      41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55
Db      493 AAGTACCACCTCTATGTTTAAAGGTTCTTTGAGCAGGTTTCTGGAAAAGAACAGCA 552
Qy      56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
Db      553 GCCAAAATGCCATATGATGATGACTGTGGAATCCATGCCAGAGATGGATCTCTCTGCT 612
Qy      76 PheCysLeuTrpPheIleGlyHis----- 83
Db      613 TTCTGCTGTGTGTTTCATAGGCCATATACTCAATTTCTATGGGATAATAGGCAATATACC 672
Qy      83 ----- 83
Db      673 AATCTCTGAGGCTTGCGATTTCTATGTTATGCGGTGGTTATGTGGATGGTTATGAC 732
Qy      84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
Db      733 TACTCATGAAAAAGAAATCGAATGTGGAGAAAGAACCGTTCTTCTATGCGAACAAATCAT 792
Qy      99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisIleTrpCysGluGluGlyAla 118
Db      793 TGCATCGGAACAGACCTGAATAGGAACCTTGTCTTCCAAACACACTGGTGTGAGGAAGGTGCA 852
Qy      119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
Db      |

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Db      853 TCAGTTTCCTCATGCTCGGAAACCTACTGTGGACTTTATCTCTGAGTCAGAACCAAGATG 912
Qy      139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
Db      913 AAGCAGTGGCTAGTTTCTTTGAGAAGAAATATCAACCCAGATTAAAGCATACATCAGCATG 972
Qy      159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
Db      973 CATTTCATACCTCCAGCATATAGTGTTCCTATATTCCTATACAGAGTAAAGCAAGAC 1032
Qy      179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
Db      1033 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTCTGCTATTGAGAAAATTAGTAAA 1092
Qy      199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
Db      1093 AATACCAGGTATACACATGGCCATGGCTCAGAAACCTTATACCTAGCTCCTCGGAGGTGGG 1152
Qy      219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db      1153 GACGATTGGATCTATGATTTGGGCAATCAAAATATTCGTTTACAATTGAACCTTCGAGATACG 1212
Qy      232 -----ThrSerAsnProProValGluLysLeuLe 241
Db      1213 GGCACATACGATTCCTGCTGCCGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTT 1272
Qy      241 uProLeuSerLeuLys 246
Db      1273 GCGCTGCTCTAAAA 1288

RESULT 5
US-10-115-479-67
; Sequence 67, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Caaman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934

```



```
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 67
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1304)
US-10-115-479-67

Alignment Scores:
Pred. No.: 4,12e-154 Length: 1743
Score: 1248.50 Matches: 244
Percent Similarity: 79.74% Conservative: 0
Best Local Similarity: 79.74% Mismatches: 2
Query Match: 93.31% Indels: 60
DB: 16 Gaps: 3

US-09-980-881A-4 (1-246) x US-10-115-479-67 (1-1743)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 362 GCCTCCGCATCTACTATGACAGATATCACTCAATAATGAATCTATTCTTTGGATAGAA 421
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 422 TTATTAACCTGAGAGGCATCTGATATGCTTACAAAATCCCATTTGGATCCTCATTTGAG 481
Qy 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55
Db 482 AAGTACCCACTCTATGTTTAAAGGGTTCTTTGACGAGCTTCTTGAAAAGAACAGCA 541
Qy 56 AlaLysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAla 75
Db 542 GCCAAAATGCCATATGGATTGACTGTGGAATCCATGCCAGAGAAATGGATCTCTCCTGCT 601
Qy 76 PheCysLeuTrpPheIleGlyHis----- 83
Db 602 TTCTGCTTGGTTTCATAGGCCATATAAATCAATCTATGGGATAATAGGGCAATATACC 661
Qy 83 ----- 83
Db 662 AATCTCTGAGGCTTGTGGATTTCTATGTTATGCCAGTGTGTAATGGATGTTATGAC 721
Qy 84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
Db 722 TACTCATGNAAGAAATCGAATGTGGAGAAAGAACCGTTCTTTCTATGGAACATCAT 781
Qy 99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118
Db 782 TGCATCGAAGACACCTGAATAGAACTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCA 841
Qy 119 SerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
Db 842 TCCAGTTCTCTCGGAACCTACTGTGGACTTTATCTGAGTCAGAACACAGAGTG 901
Qy 139 LysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
Db 902 AAGCAGTGGCTAGTTCTTGGAGAGAAATATCAACCAGATTAAGCATACATCAGCATG 961
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Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
Db 962 CATTCATACTCCAGCATATAGTGTTCCTATATCTATATACAGCAAGTAAAGCAAGAC 1021
Qy 179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
Db 1022 CATGAGGAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTTGAGAAATTAGTAA 1081
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGly 218
Db 1082 AATACCAGGTATACATGGCCATGGCTCAGAAACCTTATACCTAGCTCTCTGGAGGTGG 1141
Qy 219 AspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 1142 GACCATTTGGATCTATGATTTGGGCATCAAAATATTCTGTTTACAATTTGAACCTTCGAGATACG 1201
Qy 232 -----ThrSerAsnProProValGluLysLeuLe 241
Db 1202 GGCACATACGGATTTCTTGTCTCCGAGCGTTTACATCAAAACCCACCTGTAGAGAAAGCTTTT 1261
Qy 241 uProLeuSerLeuLys 246
Db 1262 GCCGTGCTCTTAA 1277

RESULT 6
US-10-379-836-1
; Sequence 1, Application US/10379836
; Publication No. US20030215850A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON
; FILE REFERENCE: TAFI
; CURRENT APPLICATION NUMBER: US/10/379,836
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: U.S. 60/361,523
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Papio hamadryas
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1269)
US-10-379-836-1

Alignment Scores:
Pred. No.: 7,14e-145 Length: 1272
Score: 1177.00 Matches: 228
Percent Similarity: 78.41% Conservative: 8
Best Local Similarity: 75.75% Mismatches: 10
Query Match: 87.97% Indels: 55
DB: 15 Gaps: 2

US-09-980-881A-4 (1-246) x US-10-379-836-1 (1-1272)

Qy 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 343 GCCTCCGCATCTACTATGACAGATATCACTCAATAATGAATCTATTCTTTGGATAGAA 402
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 403 CTATAACCTGAGAAGTATCTCTGATATGCTTACAAAATCCATTTGGATCTCTCTATGAG 462
Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 463 AAGCACCACCTTTATGTTTAAAGGTTCTGGAAGAACAAACAGCCAAATGCAATG 522
Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
```

Db 523 TGGATTGACTGTGGAATCCAGCAGAAATGGATCTCCCTGCTTCTTGCTTGTGGTTC 582  
Qy 81 IleGlyHis----- 83  
Db 583 ATAGGCCATATACTGAATCTACGGGATAATAGGGAATATACCAATCTTCTGAGGCAT 642  
Qy 83 ----- 83  
Db 643 GTGGAATTTCTATGTTATGTCAGTGGTTAATGTGGAATGTTATGACTACTCATGAGAAAG 702  
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103  
Db 703 AATCGAATGTGGAAGAAGACCGTCTTCTTATCGGAACATCGTTGCATCGGAACAGAC 762  
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123  
Db 763 CTGAACAGGAACCTTGGCTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTTCTCATGC 822  
Qy 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143  
Db 823 TCGGAACCTACTGTGGACTTTATCTCGAGTCAGAACCCAGGAAGCGGCTGCTAAT 882  
Qy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163  
Db 883 TTCTTGAGAAGAAATATCAACCAATTAAGCATACATCAGCATGCATTATATCTCCAG 942  
Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183  
Db 943 CATATCGTGTTCATATCTCTATCTCGAAGCAAAAGCAACACGAGGAATTTGTCT 1002  
Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203  
Db 1003 CTAGTAGCCAGTGAAGCAGTTCGTGCTATTTCAGAAAACCCAGTAAATAATATACAGTATACA 1062  
Qy 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223  
Db 1063 CATGGCCGTGGCTCAGAAACCTTATACCTAGCTCTCGAGGTGGCGAGTTGGATCTAT 1122  
Qy 224 AspLeuGlyIleLysTyrSerPhe----- 231  
Db 1123 GATTGGGCATCAATATTCGTTTACAATTCGAGATACGGGCAAAATACGGATTC 1182  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 1183 TTGCTGCTGAGCTTACATCAAAACCCACTTGTAAAGACGCTTTTGGCGTGTCTCTAAA 1242  
Qy 246 s 246  
Db 1243 A 1243

## RESULT 7

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Patent No. US2002004941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (25)

; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

## Alignment Scores:

Pred. No.: 1.99e-108 Length: 1400  
Score: 902.00 Matches: 181  
Percent Similarity: 76.05% Conservative: 0  
Best Local Similarity: 76.05% Mismatches: 1  
Query Match: 67.41% Indels: 56  
DB: 9 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

Qy 65 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83  
Db 10 GGAATCCATGCCAGANAATGGATCTCTCTGCTTTCTGCTTGTGGTTTCATAGGCCATATA 69  
Qy 83 ----- 83  
Db 70 ACTCAATTTCTATGGGATAATAGGGCAATATACCAATCTCTGAGGCTTGTGGATTTCTAT 129  
Qy 84 -----AsnArgMetTr 87  
Db 130 GTTATGCGGTGGTTAATGTGGATGGTTATGAACACTCATCGAAAAAGAAATCGAATGTG 189  
Qy 87 pArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAs 107  
Db 190 GAGAAAGAACCGTTCCTTCTATCGAACCAATATTCATCGAACACAGACCTGAATAGGAA 249  
Qy 107 nPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerCysSerGluThrTy 127  
Db 250 CTTTGCTTCCAAACACTGGTGTGAGGAAGGTGCATCCAGTTCCTCATGCTCGGAACCTA 309  
Qy 127 rCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAr 147  
Db 310 CTGTGACTTTATCTGAGTCAGAACCCAGAAAGTGAAGCAGTGGTAGTTCTTTGAGAAG 369  
Qy 147 gAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPh 167  
Db 370 AAATATCAACAGATTAAAGCATACATCAGCATGCATTCATCTACTCCAGCATATAGTGT 429  
Qy 167 eProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSe 187  
Db 430 TCCATATTTCTATACAGAAAGTAAAGCAAGCAACATGAGAAACTGTCTCTAGTAGCAG 489  
Qy 187 rGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisG1 207  
Db 490 TGAAGCAGTTCTGTCTATTGAGAAACTAGTAAAAATACCAGGTATATACATGSCCATGG 549  
Qy 207 ySerGluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGly11 227  
Db 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTTGGGCAT 609  
Qy 227 eLysTyrSerPhe----- 231  
Db 610 CAAATATTTCTGTTTACAAATTGAACTTCGAGATACGGGCACATACGGATTCTTGTGCGGA 669  
Qy 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246  
Db 670 GCGTTACATCAAAACCCACCTGTAGAGAAGCTTTTGGCGTGTCTCTATAAA 719

## RESULT 8

US-09-925-302-24  
; Sequence 24, Application US/09925302  
; Publication No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 896  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 24  
;; LENGTH: 1400  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (25)  
;; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-302-24

Alignment Scores:  
Pred. No.: 1.99e-108 Length: 1400  
Score: 902.00 Matches: 181  
Percent Similarity: 76.05% Conservative: 0  
Best Local Similarity: 76.05% Mismatches: 1  
Query Match: 67.41% Indels: 56  
DB: 10 Gaps: 2

US-09-980-881A-4 (1-246) x US-09-925-302-24 (1-1400)

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Qy 65 GlylleHieAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis--- 83
Db 10 GGATCCATGCCAGAAATGGATCTCTCTGCTTTCTGCTTGTGTTTCATAGCCCATATA 69
Qy 83 ----- 83
Db 70 ACTCAATTCATGGGATAATAGGCAATATACCAATCTCTCGAGGCTTGTGATTTCAT 129
Qy 84 -----AsnArgMetTr 87
Db 130 GTTATGCCGGTGTTAATCTGGATGTTATGAACACTCATCGAAAAAGAAATCGAATGG 189
Qy 87 pArglyAsnArgSerPheTyAlaAsnAenHisCysIleGlyThrAspLeuAsnArgAs 107
Db 190 GAGAAGAACCGTTCTTTCTATGCGAACCAATATTGATCGGACAGACCTGAATAGGAA 249
Qy 107 nPheAlaSerLyseHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTy 127
Db 250 CTTTGTCTTCCAAACACTGCTGTGAGGAGTGATCCAGTCTCTCATGCTCGAAACCTA 309
Qy 127 rCysGlyLeuTyProGluSerGluProGluVallylsAlaValAlaSerPheLeuArgAr 147
Db 310 CTGTGGACTTTATCTCTGAGTCAAGAACGAGGAGGAGGAGGAGTGTCTTCTTGAGAAG 369
Qy 147 gAenlleAsnGlnIleLysAlaTyIleSerMetHisSerTySerGlnHisIleValPh 167
Db 370 AATATCAACCAAGATTAAAGCATACATCAGCATGCAATTCATCTCCAGCATATAGTGT 429
Qy 167 eProTySerTyThrArgSerLyssSerLyssAspHisGluGluLeuSerLeuValAlaSe 187
Db 430 TCCATATTCCTATACACGAAGTAAAGCAAGACCATGAGGAACCTGCTCTAGTAGCCAG 489
Qy 187 rGluAlaValArgAlaIleGluLyThrSerLyssAsnThrArgTyThrHisGlyHisGl 207
Db 490 TGAAGCAGTTCGTGCTATTGAGAAAACTAGTAAAAATACCAAGTATACACATGGCCG 549
Qy 207 ySerGluThrLeuTyLeuAlaProGlyGlyGlyAspAspTrpIleTyAspLeuGlyI 227
Db 550 CTCAGAAACCTTATACCTAGCTCTCTGAGGTGGGACGATTGGATCTATGATTGGGCAT 609
Qy 227 eLystrTySerPhe----- 231
Db 610 CAATATTCGTTTACAATTGAACCTTCGAGATACGGGCACATACGGATTCTTGTGCGCGA 669
Qy 232 -----ThrSerAsnProProValGluLyLeuLeuProLeuSerLeuLys 246
Db 670 GCGTTACATCAAAACCCACCTGTGAGAAGCTTTTGGCGCTGTCTCTTAAAA 719
```

RESULT 9

US-10-115-479-63  
;; Sequence 63, Application US/10115479  
;; Publication No. US20040006205A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Li, Li  
;; APPLICANT: Gerlach, Valerie L.  
;; APPLICANT: Liu, Xiaohong  
;; APPLICANT: Miller, Charles E.  
;; APPLICANT: Spytek, Kimberly A.  
;; APPLICANT: Zerhusen, Bryan D.  
;; APPLICANT: Pena, Carol E.A.  
;; APPLICANT: Shenoy, Suresh G.  
;; APPLICANT: Zhong, Haihong  
;; APPLICANT: Smithson, Glendda  
;; APPLICANT: Casman, Stacie J.  
;; APPLICANT: Boldog, Perenc L.;  
;; APPLICANT: Voss, Edward  
;; APPLICANT: Vernet, Corine  
;; APPLICANT: MacDougall, John A.  
;; APPLICANT: Rastelli, Luca  
;; APPLICANT: Anderson, David W.  
;; APPLICANT: Zhong, Mei  
;; APPLICANT: Mezes, Peter S.  
;; APPLICANT: Furtak, Katarzyna  
;; APPLICANT: Patturajan, Meera  
;; APPLICANT: Burgess, Catherine E.  
;; APPLICANT: Malyanker, Uriel M.  
;; APPLICANT: Shimkets, Richard A.  
;; APPLICANT: Taupier, Raymond J.  
;; APPLICANT: Edinger, Shlomit R.  
;; APPLICANT: Mazur, Ann  
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
;; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
;; CURRENT APPLICATION NUMBER: US/10/115,479  
;; CURRENT FILING DATE: 2002-11-18  
;; PRIOR APPLICATION NUMBER: 60/281,136  
;; PRIOR FILING DATE: 2001-04-03  
;; PRIOR APPLICATION NUMBER: 60/281,863  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/281,906  
;; PRIOR FILING DATE: 2001-04-05  
;; PRIOR APPLICATION NUMBER: 60/282,934  
;; PRIOR FILING DATE: 2001-04-10  
;; PRIOR APPLICATION NUMBER: 60/283,657  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,678  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,687  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/283,710  
;; PRIOR FILING DATE: 2001-04-13  
;; PRIOR APPLICATION NUMBER: 60/284,234  
;; PRIOR FILING DATE: 2001-04-17  
;; PRIOR APPLICATION NUMBER: 60/285,325  
;; PRIOR FILING DATE: 2001-04-19  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 198  
;; SEQ ID NO 63  
;; LENGTH: 1037  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (41)..(1007)  
US-10-115-479-63  
Alignment Scores:  
Pred. No.: 2.45e-104 Length: 1037  
Score: 869.50 Matches: 180  
Percent Similarity: 68.18% Conservative: 0  
Best Local Similarity: 68.18% Mismatches: 2  
Query Match: 64.99% Indels: 82  
DB: 16 Gaps: 2

```

US-09-980-881A-4 (1-246) x US-10-115-479-63 (1-1037)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 383 GCCTCCGCATCGTACTATGAACAGATATCACTCACTAAATGAATCTATTCTTGATAGAA 442
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 443 TTTATAACTGAGAGGCATCCTGATATGTTTCAAAAAATCCATCGATCGATCCTCATTTGAG 502
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 503 AAGTACCACCTCTATGTTTAAAGGTTTCTGAAAAGAACAGCAGCCAAAAATGCCATA 562
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 563 TGGATTGAC----- 571
QY 81 IleGlyHisAsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIle 100
Db 571----- 571
QY 101 GlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSer 120
Db 571----- 571
QY 121 SerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAla 140
Db 572-----TGTGGACTTTTATCTCTGAGTCAGAACCCAGAAAGTGAAGCA 610
QY 141 ValAlaSerPheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSer 160
Db 611 GTGGCTAGTTTCTTGAGAAGAATAATCAACCAGATTAAAGCATATACATCAGCATCATCA 670
QY 161 TyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGlu 180
Db 671 TACTCCAGCATATAGTGTTCATATTCCTATACAGAAATAAGCAAGACCATGAG 730
QY 181 GluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThr 200
Db 731 GAACCTGCTCTAGTAGCCAGTGAAGCAGTTCGTGCTATTGAGAAAAATTAGTAAAAATACC 790
QY 201 ArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyAspAsp 220
Db 791 AGGTATACACATGGCCATGGCTCAAAACCTTATACCTAGCTCTCTGGAGGTGGGGACGAT 850
QY 221 TrpIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 851 TGGATCTATGATTGGGCATCAATATTCGTTTACAATTGAACTTCGAGATACGGGCACA 910
QY 232-----ThrSerAsnProProValGluLysLeuLeuProLe 243
Db 911 TACGATTCTTGTCCGGAGCGTTACATACATCAACCCACCTGTAGAGAAGCTTTTGGCGCT 970
QY 243 uSerLeuLys 246
Db 971 GTCTCTAAAA 980
RESULT 10
US-10-115-479-65
; Sequence 65, Application US/10115479
; Publication No. US2004000620SAI
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong

```

```

; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 65
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1103)
; US-10-115-479-65
Alignment Scores:
Pred. No.: 4,07e-99 Length: 1132
Score: 830.50 Matches: 171
Percent Similarity: 55.88% Conservative: 0
Best Local Similarity: 55.88% Mismatches: 1
Query Match: 62.07% Indels: 134
DB: 16 Gaps: 4
US-09-980-881A-4 (1-246) x US-10-115-479-65 (1-1132)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
Db 383 GCCTCCGCATCGTACTATGAACAGATATCACTCACTAAATGAATCTATTCTTGATAGAA 442
QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 443 TTTATAACTGAGAGGCATCCTGATATGCTTACAAAAATCCACATTCGATCCTCATTTGAG 502
QY 41 LysTyrProLeuTyrValLeuLys-----ValSerGlyLysGluGlnThr 55

```

```
Db 503 AAGTACCACCTCTATGTTTAAAGGGTTCTTTTGAGCAGAGTTTCTGGAAGAACACAGCA 562
Qy 56 AlaLysAsnAlaIleThrPheLeuSerCysGlyLeuHisAlaArgGluThrPheLeuSerProAla 75
Db 563 GCCAAAAATGCCATATGGATTCAGTGTGAATCCATGCCAGAGAAATGGATCTCTCTGCT 622
Qy 76 PheCysLeuThrPheLeuGlyHis 83
Db 623 TTTCTGTTGTTTCATAGCCCATATACTCAATTCATGAGTAATAGGGCAATATACC 682
Qy 83 ----- 83
Db 683 AATCTCTGAGGCTTGATTTCTATGTTATGCCGGTGGTTAAATGTGGATGTTATGAC 742
Qy 84 -----AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHis 98
Db 743 TACTCATGAAAAAGAAATCGAATGGAGAAAGAACCGTTCTTCTATGCGAACAATCAT 802
Qy 99 CysIleGlyThrAspLeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAla 118
Db 803 TGCATCGGAACAGACCTGATAGGAACCTTGTCTCCAAACACTGGTGTGAGGAAGTGCA 862
Qy 119 SerSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGluSerGluProGluVal 138
Db 863 TCCAGTTCTCTATGCTCGGAACCTACTGTGGACTTTATCTCAG----- 907
Qy 139 LysAlaValAlaSerPheLeuArgAsnIleAsnGlnIleLysAlaTyrIleSerMet 158
Db 907 ----- 907
Qy 159 HisSerTyrSerGlnHisIleValPheProTyrSerTyrThrArgSerLysSerLysAsp 178
Db 907 ----- 907
Qy 179 HisGluGluLeuSerLeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLys 198
Db 907 ----- 907
Qy 199 AsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGly 218
Db 908 -----TCAGAAACCTTATACCTAGCTCTCGAGGTGG 940
Qy 219 AspAspTyrIleTyrAspLeuGlyIleLysTyrSerPhe----- 231
Db 941 GACGATGGATCTATGATTTGGCATCAAAATATTCGTTTACAAATTCGAATTCGAGATACG 1000
Qy 232 -----ThrSerAsnProProValGluLysLeuLeu 241
Db 1001 GGCACATACGATTCCTGCTGCGGAGCGTTACATCAAAACCCACCTGTAGAGAAGCTTTT 1060
Qy 241 uProLeuSerLeuLys 246
Db 1061 GCGGCTGTCTCTAAAA 1076
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## RESULT 11

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US-10-477-515-1
; Sequence 1, Application US/10477515
; Publication No. US20040136976A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN ZINC CARBOXYPEPTIDASE B-LIKE PROTEIN
; FILE REFERENCE: LIOJ55 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/477,515
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US 60/292,329
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-515-1
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## Alignment Scores:

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Pred. No.: 8.98e-63 Length: 1302
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 17 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-477-515-1 (1-1302)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArg 25
Db 406 TATGAAGTTTATCACTCTCTAGAAAGAAATCAAAATGGATGGATCATCTGAAATAAAACT 465
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 466 CACTCAGCCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT 525
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
Db 526 ATTTTAAAGCTG--GGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGCT 582
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 583 ATTCAATGCAAGAGAATGGATTTGGTCTGCTCTTTTGTCTAGTGGTGTGTAAGAAAGACTCTT 642
Qy 81 ----- 81
Db 643 CTAACATATAAGAGTGACCCAGCCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702
Qy 82 -----GlyHisAsnArgMetTrpArg 88
Db 703 ATGCTGTGTTTAACTGCGATGATACCATTTTGTGGACCAATGATCGATTTTGGAGA 762
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 763 AAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCGGTGGAGTGGATGCCAATAAGAACTGG 822
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerSerSerSerSerSerSerSer 128
Db 823 AAAGTGAAG---TGTGTGTGATGAAGAGCTTCTATGCACCTTGTGTGATGACACATCTGT 879
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 880 GGCCTCTTTCCAGATCTGAGCCGGAAGTGAAGGCTGTAGCTTAATCTCTCGAAAAACAC 939
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 940 AGAAAGCACATTTAGGGCTTATCTCTCTTTCATGTCATATGCTCAGATGTTACTGTATCCC 999
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 1000 TATCTTCAAAATATGCAACATTTCCCAATTTTAGATGTGTGGAAATCTGCAGCTTATAAA 1059
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1060 GCTGTGAATGCACTTCAGTCAGTA---TACGGGGTACGATACAGATATGAGCAGCCTCC 1116
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1117 ACAACGTTGTATGTGAGCTCTGCTAGCTCAATGGATTTGGGCTACAAAAAATGGAATACCT 1176
Qy 229 TyrSerPhe----- 231
Db 1177 TATGCAATTTGCTTTTCCAACTACGTGACACTGTGATATTTTGGATTTTCTCCAGAGATG 1236
Qy 232 -ThrSerAsnProProValGluLysLeu 240
Db 1237 CTCATCAAAACCCCTCTACAGAAACTA 1264

RESULT 12
US-10-200-344-9
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; Sequence 9, Application US/10200344
; Publication No. US20020173641A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020173641A1el Human Carboxypeptidases and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0047-USA
; CURRENT APPLICATION NUMBER: US/10/200,344
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US/09/675,305
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-200-344-9

Alignment Scores:
Pred. No.: 9,08e-63 Length: 1311
Score: 556.50 Matches: 113
Percent Similarity: 53.45% Conservative: 42
Best Local Similarity: 38.97% Mismatches: 77
Query Match: 41.59% Indels: 58
DB: 13 Gaps: 5

US-09-980-881A-4 (1-246) x US-10-200-344-9 (1-1311)

Qy 6 TyrGluGlnTyrHisSerLeuAsnGluileTyrSerTrpIleGluPheIleThrGluArg 25
Db 406 TATGAAGTTTATCACTCTTGAAGAAATTCAAAATTCGATCATCTCGAATAAACT 465
Qy 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
Db 466 CACTCAGCGCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT 525
Qy 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGly 65
Db 526 ATTTTAAAGCTG---GGCAGAGATCAGCATCAAGAGCTGTTGGATAGACTGTGGT 582
Qy 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
Db 593 ATTCATGCAAGAGATGATGGTCTGCTGCTTTTGTCAAGTGGTTTGTAAAGAAAGCTCTT 642
Qy 81 ----- 81
Db 643 CTAACATATAAGAGTGACCCAGCCATGAGAAAAATGTTGAATCATCTATATTTCTATATC 702
Qy 82 -----GlyHisAsnArgMetTrpArg 88
Db 703 ATGCGCTGTGTTAACTGCATGGATACCATTTTAGTTGGACCAATGATCGATTTTGGAGA 762
Qy 89 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 108
Db 763 AAAACAAGGTCAAGGAATCAAGGTTTCGCTGCGGTGGAGTGGATGCCAATAGAAACTGG 822
Qy 109 AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCys 128
Db 823 AAAGTGAAG---TGGTGTGATGAAGAGCTTCTATGCACCCCTTGTGATGCACATACCTGT 879
Qy 129 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 148
Db 880 GGCCCTTTTCAGAAATCTGAGCCGGAAGTGAAGCTGTAGCTAATCTTCGAAACAC 939
Qy 149 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 168
Db 940 AGAAAGCACATTAGGGCTTATCTCTCTCTTTTCATGCATATGTCATGATGTTACTGTATCCC 999
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Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu 188
Db 1000 TATCTTTCAAAATATGCAACAATTTCCCAATTTTAGATGTGTGGAATCTGCAGCTTATAAA 1059
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1060 GCTGTGAATGCATCTCAGTCAGTA---TAGGGGTAGCATACAGATATGACCAAGCTCC 1116
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1117 ACAACGTTGTATGTAGCTCTGCTCAATGATGGCGCTACAAAAATGGAATACCT 1176
Qy 229 TyrSerPhe----- 231
Db 1177 TATGCATTTGCTTCGAACTACGTGACACTGGATATTTTGGATTTTACTCCCCAGATG 1236
Qy 232 -ThrSerAsnProValGluLysLeu 240
Db 1237 CTCAATCAACCCACTGTACAGAACTA 1264

RESULT 13
US-10-274-639-33
; Sequence 33, Application US/10274639
; Publication No. US20030232349A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELESEANE, Angelo M.; GANDHI, Ameena R.
; APPLICANT: HAPALIA, April J.A.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra; TRIBOULEY, Catherine M.
; APPLICANT: DAS, Debopriya; KALLICK, Deborah A.
; APPLICANT: NGUYEN, Darniel B.; LEE, Ernestine A.
; APPLICANT: KHAN, Farrah A.; YUE, Henry
; APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.
; APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Juming; THANGAVELU, Kavitha
; APPLICANT: DING, Li; KEARNEY, Liam
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.
; APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
; APPLICANT: BURFORD, Neil; WALIA, Narinder K.
; APPLICANT: LAL, Preeti G.; LEE, Sally
; APPLICANT: TODD, Stephen; LO, Terence P.
; APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.
; APPLICANT: AZIMZAI, Valda; LU, Yan
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0167 USA
; CURRENT APPLICATION NUMBER: US/10/274,639
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/22397
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/220,063
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,680
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,544
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,717
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/225,988
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/227,568
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1993
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030232349A1 4948403CB1
US-10-274-639-33
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Alignment Scores:		1-78e-62	Length:	1993
Pred. No.:	Score:	556.50	Matches:	113
Percent Similarity:		53.45%	Conservative:	42
Best Local Similarity:		38.97%	Mismatches:	77
Query Match:		41.59%	Indels:	58
DB:		15	Gaps:	5
US-09-980-881A-4 (1-246) x US-10-274-639-33 (1-1993)				
Qy	6	TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg	25	
Db	743	TATGAAGTTTATCACTCTCTAGAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT	802	
Qy	26	HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr	45	
Db	803	CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT	862	
Qy	46	ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly	65	
Db	863	ATTTTAAAGCTG---GGCAGACGATCAGCACTCAAAGAGCTGTTGGATAGACTGTGT	919	
Qy	66	IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	81	
Db	920	ATTCATGCAAGAGATGGATGCTGCTGCTTTTGTCTGCTGCTTTGTTGTAAGAAAGCTTT	979	
Qy	81	-----	81	
Db	980	CTAACATATAAGAGTGACCCGACCATGAGAAAAATGTTGAATCATCTATATTTCTATATC	1039	
Qy	82	-----GlyHisAsnArgMetTrpArg	88	
Db	1040	ATGCCCTGTGTTTAACGTCGATGATACCAATTTTAGTTGGACCAATGATCGATTTGGAGA	1099	
Qy	89	LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe	108	
Db	1100	AAAAAAGGTCAGGAACCTCAAGGTTTCGTCGCGTGAGTGATGATGCCAATAGAAACTGG	1159	
Qy	109	AlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerSerLysTrpCys	128	
Db	1160	AAAGTGAAG---TGGTGTGATGAAGGAGCTTCTATGCACCCCTTGTGATCAGACATACCT	1216	
Qy	129	GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn	148	
Db	1217	GGCCCTTCCAGAAATCAGCCGGAAGTGAAGGCTGTAGCTTAACCTCTCGAAACAC	1276	
Qy	149	IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro	168	
Db	1277	AGAAAGCACATTAGGGCTTATCTCTCTCTTCATGTCATATGCTCAGATGTTACTGTATCC	1336	
Qy	169	TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu	188	
Db	1337	TATTTCTTACAAATATGCAACAATTCCTCAATTTTAGATGTGTGGAATCTCGAGCTTATAA	1396	
Qy	189	AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer	208	
Db	1397	GCTGTGAATGCATTCAGTCAGTA---TACCGGGTAGATACAGATATGAGCAGCTCC	1453	
Qy	209	GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys	228	
Db	1454	ACAACGTTGTGTGAGCTCTGTAGCTCAATGATGATGGCCCTTACAAAATGGAATACCT	1513	
Qy	229	TyrSerPhe-----	231	
Db	1514	TATGCATTTCTTTTCGAACCTACGTCAGCTGGATATTTTGGATTTTACTCCAGAGATG	1573	
Qy	232	-ThrSerAsnProProValGluLysLeu	240	
Db	1574	CTCATCAACCCACCTGTATCAGAAACTA	1601	
RESULT 14				
US-10-333-574-33				
; Sequence 33, Application US/10333574				
Publication No. US20040091962A1				
GENERAL INFORMATION:				
APPLICANT: INCYTE GENOMICS, INC.				
APPLICANT: DELEGANE, Angelo M.; GANDHI, Ameena R.				
APPLICANT: HAPALIA, April J.A.; LU, Dyrung Aina M.				
APPLICANT: ARVIZO, Chandra S.; TRIBOULEY, Catherine M.				
APPLICANT: DAS, Debopriya; KALLICK, Deborah A.				
APPLICANT: NGUYEN, Damiel B.; LEE, Ernestine A.				
APPLICANT: KHAN, Farrah A.; YUE, Henry				
APPLICANT: AU-YOUNG, Janice K.; GRIFFIN, Jennifer A.				
APPLICANT: POLICKY, Jennifer L.; RAMKUMAR, Jayalaxmi				
APPLICANT: YANG, Junning; THANGAVELU, Kavitha				
APPLICANT: DING, Li; KEARNEY, Liam				
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.				
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.				
APPLICANT: BURFORD, Neil; CHAWLA, Narinder K.				
APPLICANT: LAL, Preeti G.; LEE, Sally				
APPLICANT: TODD, Stephen; LO, Terence P.				
APPLICANT: TANG, Y. Tom; ELLIOTT, Vicki S.				
APPLICANT: AZIMZAI, Yalda; LU, Yan				
TITLE OF INVENTION: PROTEASES				
FILE REFERENCE: PI-0167 USN				
CURRENT APPLICATION NUMBER: US/10/333,574				
CURRENT FILING DATE: 2003-01-21				
PRIOR APPLICATION NUMBER: US 01/22397				
PRIOR FILING DATE: 2001-07-17				
PRIOR APPLICATION NUMBER: US 60/220,063				
PRIOR FILING DATE: 2000-07-21				
PRIOR APPLICATION NUMBER: US 60/221,680				
PRIOR FILING DATE: 2000-07-28				
PRIOR APPLICATION NUMBER: US 60/223,544				
PRIOR FILING DATE: 2000-08-04				
PRIOR APPLICATION NUMBER: US 60/224,717				
PRIOR FILING DATE: 2000-08-11				
PRIOR APPLICATION NUMBER: US 60/225,988				
PRIOR FILING DATE: 2000-08-16				
PRIOR APPLICATION NUMBER: US 60/227,568				
PRIOR FILING DATE: 2000-08-23				
NUMBER OF SEQ ID NOS: 42				
SOFTWARE: PERL Program				
SEQ ID NO 33				
LENGTH: 1993				
TYPE: DNA				
ORGANISM: Homo sapiens				
FEATURE:				
NAME/KEY: misc_feature				
OTHER INFORMATION: Incyte ID No: 4948403CB1				
US-10-333-574-33				
Alignment Scores:		1-78e-62	Length:	1993
Pred. No.:	Score:	556.50	Matches:	113
Percent Similarity:		53.45%	Conservative:	42
Best Local Similarity:		38.97%	Mismatches:	77
Query Match:		41.59%	Indels:	58
DB:		16	Gaps:	5
US-09-980-881A-4 (1-246) x US-10-333-574-33 (1-1993)				
Qy	6	TyrGluGlnTyrHisSerLeuAsnGluLeuTyrSerTrpIleGluPheIleThrGluArg	25	
Db	743	TATGAAGTTTATCACTCTCTAGAGAAATTCAAAATTGGATGCATCATCTGAATAAAACT	802	
Qy	26	HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr	45	
Db	803	CACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATCTCTTTT	862	
Qy	46	ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly	65	
Db	863	ATTTTAAAGCTG---GGCAGACGATCAGCACTCAAAGAGCTGTTGGATAGACTGTGT	919	
Qy	66	IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle	81	
US-10-333-574-33				
; Sequence 33, Application US/10333574				





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Db 1156 AGAAGCACATTAGGCTTATCTCTCTTTTCATGCATATGCTCAGATGTTACTGTATCCC 1215
Qy 169 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 188
Db 1216 TATTCCTTACAAATATGCAACAATTCCTCAATTTTAGATGTGGAAATCTGCAGCTTATAAA 1275
Qy 189 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 208
Db 1276 GCTGTGAATGCATTCAGTCAGTA--TACGGGGTACGATACAGATATGGACCAGCTCC 1332
Qy 209 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 228
Db 1333 ACAACGTTGTATGTAGCTCTGTAGCTCAATGGATTGGCCCTACAAAAATGGAATACCT 1392
Qy 229 TyrSerPhe----- 231
Db 1393 TATGCATTTGCTTTCGAACTACGTGACACTGGATATTTTGGATTTTACTCCAGAGATG 1452
Qy 232 -ThrSerAsnProValGluLysLeu 240
Db 1453 CTCATCAAAACCCACCTGTACAGAACTA 1480

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